

SQ Sequence 501 AA;  
Query Match 100.0%; Score 3662; DB 1; Length 501;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 MRLPKLLTFLWYLAWLDEFTCTVLGAPDLGQRPGQTRPGLAKAEAKERPPLARNVFRP 60  
QY 1 MRLPKLLTFLWYLAWLDEFTCTVLGAPDLGQRPGQTRPGLAKAEAKERPPLARNVFRP 60  
Db 61 GGHSGGGATNANARAKGGTGTGGLTQPKKDEPKKLPDPGPGPKPGHPQTRQATAR 120  
QY 61 GGHSGGGATNANARAKGGTGTGGLTQPKKDEPKKLPDPGPGPKPGHPQTRQATAR 120  
Db 121 TVTPKGQLPGGKAPPKAGSVSSFLKKAREPGPPREPKEPRPPPIITPHEYMLSLYRTL 180  
QY 121 TVTPKGQLPGGKAPPKAGSVSSFLKKAREPGPPREPKEPRPPPIITPHEYMLSLYRTL 180  
Db 181 SDADRKGNSSVKLEAGLANITTSFIDKGQDDRGVPVRKQRYVFDISALEKDGLLGAELR 240  
QY 181 SDADRKGNSSVKLEAGLANITTSFIDKGQDDRGVPVRKQRYVFDISALEKDGLLGAELR 240  
Db 241 ILRKKPSDTAKPAAPGGGAAQLKSSCPGSRQPASLLDVRSPGLDGSWEVFIWKLF 300  
QY 241 ILRKKPSDTAKPAAPGGGAAQLKSSCPGSRQPASLLDVRSPGLDGSWEVFIWKLF 300  
Db 301 RNFKNSAQLCLELEAWERGRAVDLRLGLFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA 360  
QY 301 RNFKNSAQLCLELEAWERGRAVDLRLGLFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA 360  
Db 361 RSGQDDKTVYELFSORRKRRAPLATROGKRPKNLKAARCSKALHVNFKMGWDDWIIA 420  
QY 361 RSGQDDKTVYELFSORRKRRAPLATROGKRPKNLKAARCSKALHVNFKMGWDDWIIA 420  
Db 421 PLEYEAFHCEGLCEPPLRSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFID 480  
QY 421 PLEYEAFHCEGLCEPPLRSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFID 480  
Db 481 SANNVYKQYEDMVVESCGR 501  
QY 481 SANNVYKQYEDMVVESCGR 501

RESULT 8  
ID W19210 standard; Protein; 501 AA.  
AC W19210;  
DT 04-MAR-1998 (first entry)  
DE Human TGF-beta protein MP52.  
KW Human transforming growth factor-beta; TGF-beta; MP52; superfamily;  
KW cartilage; bone inducing activity; inhibit; bone resorption.  
OS Homo sapiens.  
PN DE19548476-A1.  
PD 26-JUN-1997.  
PR 22-DEC-1995; 048476.  
PR 22-DEC-1995; DE-048476.  
PA (BTOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.  
PI Bechtold R, Hotten G, Paulista M, Pohl J, Hoetten G;  
DR WPI; 97-333931/31.  
DR N-PSDB; T69695.  
PT Compound containing protein from TGF-beta superfamily - has bone  
PT and/or cartilage inducing activity, useful in treatment of, e.g.  
PT osteoporosis, bone damage, Paget's disease and osteoarthritis.  
PS Claim 3; Page 9; 10pp; German.  
CC This sequence is the human transforming growth factor (TGF)-beta protein  
CC designated MP52. MP52 can be used in a compound of formula (I):  
CC A-X(1-20)-B(1-20) (I): A = protein, or fragment, of the TGF-beta  
CC superfamily with cartilage and/or bone inducing activity (e.g. MP52);  
CC B = 1 or more substituent groups with an affinity to the extracellular  
CC matrix, cellular components of bone and/or cartilage and/or to a  
CC biocompatible carrier matrix; X = 1 or more covalent bonds and/or spacer  
CC groups. The compound may be used to inhibit bone resorption, prevent or  
CC treat bone or cartilage related disorders, including osteoporosis,  
CC Paget's disease, osteodystrophy, osteoarthritis or osteoarthropathy and

CC to treat bone or cartilage damage caused by wounding or overloading.  
SQ Sequence 501 AA;  
Query Match 100.0%; Score 3662; DB 1; Length 501;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 MRLPKLLTFLWYLAWLDEFTCTVLGAPDLGQRPGQTRPGLAKAEAKERPPLARNVFRP 60  
QY 1 MRLPKLLTFLWYLAWLDEFTCTVLGAPDLGQRPGQTRPGLAKAEAKERPPLARNVFRP 60  
Db 61 GGHSGGGATNANARAKGGTGTGGLTQPKKDEPKKLPDPGPGPKPGHPQTRQATAR 120  
QY 61 GGHSGGGATNANARAKGGTGTGGLTQPKKDEPKKLPDPGPGPKPGHPQTRQATAR 120  
Db 121 TVTPKGQLPGGKAPPKAGSVSSFLKKAREPGPPREPKEPRPPPIITPHEYMLSLYRTL 180  
QY 121 TVTPKGQLPGGKAPPKAGSVSSFLKKAREPGPPREPKEPRPPPIITPHEYMLSLYRTL 180  
Db 181 SDADRKGNSSVKLEAGLANITTSFIDKGQDDRGVPVRKQRYVFDISALEKDGLLGAELR 240  
QY 181 SDADRKGNSSVKLEAGLANITTSFIDKGQDDRGVPVRKQRYVFDISALEKDGLLGAELR 240  
Db 241 ILRKKPSDTAKPAAPGGGAAQLKSSCPGSRQPASLLDVRSPGLDGSWEVFIWKLF 300  
QY 241 ILRKKPSDTAKPAAPGGGAAQLKSSCPGSRQPASLLDVRSPGLDGSWEVFIWKLF 300  
Db 301 RNFKNSAQLCLELEAWERGRAVDLRLGLFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA 360  
QY 301 RNFKNSAQLCLELEAWERGRAVDLRLGLFDRAARQVHEKALFLVFGRTKKRDLFFNEIKA 360  
Db 361 RSGQDDKTVYELFSORRKRRAPLATROGKRPKNLKAARCSKALHVNFKMGWDDWIIA 420  
QY 361 RSGQDDKTVYELFSORRKRRAPLATROGKRPKNLKAARCSKALHVNFKMGWDDWIIA 420  
Db 421 PLEYEAFHCEGLCEPPLRSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFID 480  
QY 421 PLEYEAFHCEGLCEPPLRSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFID 480  
Db 481 SANNVYKQYEDMVVESCGR 501  
QY 481 SANNVYKQYEDMVVESCGR 501

RESULT 9  
ID R95635 standard; Protein; 501 AA.  
AC R95635;  
DT 25-OCT-1996 (first entry)  
DE Cartilage-derived morphogenetic protein-1.  
KW Human; cartilage-derived morphogenetic protein-1; CDMP-1;  
KW articular cartilage; chondrogenic; vulnery; implantation;  
KW chondromalacia; osteoarthritis; therapy; joint repair.  
OS Homo sapiens.  
FH Key  
FT peptide 2..19  
FT region 2..377  
FT modified\_site 189..191  
FT cleavage\_site 378..381  
FT domain 382..501  
FT peptide 388..400  
FT peptide 417..447  
FT peptide /note= "Highly conserved consensus motif (R95641)"  
PN WO9614335-A1.  
PD 17-MAY-1996.  
PF 07-NOV-1994; U12814.  
PR 07-NOV-1994; WO-U12814.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Chang SC, Luyten FP, Moos M;  
 DR WPI; 96-251714/25.  
 DR N-PSDB; T31601.  
 PT New purified cartilage extracts and proteins - used to stimulate the  
 PT development and repair of cartilage in vivo.  
 PS Claim 11; Fig 1; 34pp; English.  
 CC The sequence represents human articular cartilage-derived  
 CC morphogenetic protein-1 (CDMP-1). The protein contains a putative  
 CC transmembrane signal peptide, a pro-region, a typical proteolytic  
 CC cleavage site, and a C-terminal domain containing 7 highly  
 CC conserved Cys residues characteristic of the transforming growth  
 CC factor-beta gene family. A single N-glycosylation site is located  
 CC in the pro-region. A 13-amino-acid peptide (R95642) has been used  
 CC to raise rabbit polyclonal antibodies for screening of tissues for  
 CC CDMP-1 expression. A consensus highly conserved motif in CDMP  
 CC proteins (R95641) is present in the C-terminal domain. CDMP-1 is  
 CC present in a purified cartilage extract (claimed) which stimulates  
 CC local cartilage formation and repair when combined with a matrix  
 CC and implanted in a mammal. The protein may be used in therapy of  
 CC e.g. chondromalacia or osteoarthritis, to heal joint surfaces, or  
 CC to repair cartilage after reconstructive surgery.  
 SQ Sequence 501 AA;

Query Match 98.5%; Score 3608; DB 1; Length 501;  
 Best Local Similarity 98.4%; Pred. No. 0.00e+00;  
 Matches 493; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 1 MRLPKLLTFLWYLAWLDELICTVLGAPDLGQRPGSLAKAEKERPLARNVFRP 60  
 Qy 1 MRLPKLLTFLWYLAWLDELICTVLGAPDLGQRPGSLAKAEKERPLARNVFRP 60  
 Db 61 GGHSYGGGATNANARAKGGTGTGLTQPKKDEPKLLPPRGPGPKPGHPQTRQATAR 120  
 Qy 61 GGHSYGGGATNANARAKGGTGTGLTQPKKDEPKLLPPRGPGPKPGHPQTRQATAR 120  
 Db 121 TVTPKGQLPGGKAPPKAGSVSPSEFLKKAREPPPREPKPPPTTPHEYMLSLYRTL 180  
 Qy 121 TVTPKGQLPGGKAPPKAGSVSPSEFLKKAREPPPREPKPPPTTPHEYMLSLYRTL 180  
 Db 181 SDADRKGNSSVKLEAGLANITTSFIDKGQDDRGVPVVRKQRYVDFISALEKDGLLGAE 240  
 Qy 181 SDADRKGNSSVKLEAGLANITTSFIDKGQDDRGVPVVRKQRYVDFISALEKDGLLGAE 240  
 Db 241 ILRKKPSDTAKPAPGGGAAQLKSSCPGSRQPAALLDVRSVPLDGSNGVEFIDWKLF 300  
 Qy 241 ILRKKPSDTAKPAPGGGAAQLKSSCPGSRQPAALLDVRSVPLDGSNGVEFIDWKLF 300  
 Db 301 RNFNSAQLCLELEAWERGRAVDLRLGLGFDRAAQVHEKALFLVFGRTKKRDLEFNEIKA 360  
 Qy 301 RNFNSAQLCLELEAWERGRAVDLRLGLGFDRAAQVHEKALFLVFGRTKKRDLEFNEIKA 360  
 Db 361 RSGQDDKTVYEYLFSSQRKRRAPLNATROGKRPKNLARCCKALHVNFKDMGDDWIIA 420  
 Qy 361 RSGQDDKTVYEYLFSSQRKRRAPLNATROGKRPKNLARCCKALHVNFKDMGDDWIIA 420  
 Db 421 PLEYEAFHCEGLCEFFPLRSHLEPTNHAIVQTLNMSMDPESTPPCCVPTRLSPISILFID 480  
 Qy 421 PLEYEAFHCEGLCEFFPLRSHLEPTNHAIVQTLNMSMDPESTPPCCVPTRLSPISILFID 480  
 Db 481 SANNNVYKQYEDMVVESCGR 501  
 Qy 481 SANNNVYKQYEDMVVESCGR 501

RESULT 10  
 ID R60022 standard; Protein; 495 AA.  
 AC R60022;  
 DT 15-MAR-1995 (first entry)  
 DE Growth differentiation factor 5.  
 KW GDF-5; growth differentiation factor 5; diagnostic; therapeutic;  
 KW detection; treatment; cell proliferative disorders; uterus tissue;  
 KW skeletal tissue; uterine acoplasm; endometriosis; reagent;  
 KW suppression; transforming growth factor beta superfamily; TGF beta.

OS Mus musculus.  
 FH Key  
 FT modified\_site 183  
 FT /note= "potential glycosylation site"  
 FT 371..375  
 FT cleavage\_site  
 FT /note= "putative tetrabasic proteolytic processing  
 FT site "  
 FT 384..385  
 FT /note= "putative tetrabasic proteolytic processing  
 FT site"  
 FT  
 PN W09415949-A.  
 PD 21-JUL-1994.  
 PF 12-JAN-1994; U00657.  
 PR 12-JAN-1993; US-003144.  
 PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MED.  
 PI Huynh T, Lee S;  
 DR WPI; 94-249127/30.  
 DR N-PSDB; Q70010.  
 PT New growth differentiation factor-5 - used to develop prods. for  
 PT the detection or treatment of cell proliferative disorders of the  
 PT uterus or skeletal tissue  
 PS Claim 1; Fig 1; 79pp; English.  
 CC R60022 shows the amino acid sequence of Growth differentiation  
 CC factor 5, which is encoded by Q70010. The GDF-5 sequence contains  
 CC a core of hydrophobic amino acids near the N-terminus, suggestive  
 CC of signal sequence secretion. The sequence contains all of the  
 CC highly conserved residues present in other members of the  
 CC transforming growth factor beta superfamily, including the seven  
 CC cysteine residues with their characteristic spacing. The prods. of the  
 CC invention can be used for detection of a cell proliferative disorder  
 CC of the uterus or skeletal tissue which is associated with GDF-5  
 CC expression. Antisense sequences of GDF-5 can be used to treat uterine  
 CC neoplasm, endometriosis, or skeletal disorders (claimed). The prods.  
 CC can also be used in eg. contraception, in vitro fertilisation or in  
 CC preventing premature labour.  
 SQ Sequence 495 AA;

Query Match 91.0%; Score 3332; DB 1; Length 495;  
 Best Local Similarity 91.2%; Pred. No. 9.21e-297;  
 Matches 457; Conservative 23; Mismatches 15; Indels 6; Gaps 2;

Db 1 MRLPKLLTFLWYLAWLDELICTVLGAPDLGQRPGSLAKAEKERPLARNVFRP 60  
 Qy 1 MRLPKLLTFLWYLAWLDELICTVLGAPDLGQRPGSLAKAEKERPLARNVFRP 60  
 Db 61 GGHYIGVATNA--RAGSSQGT----QAKKDEPKMPRRSGGSETKPGSPQTRQAAAR 114  
 Qy 61 GGHSYGGGATNANARAKGGTGTGLTQPKKDEPKLLPPRGPGPKPGHPQTRQATAR 120  
 Db 115 TVTPKGQLPGGKASSKAGSAPSSFLKKTRTPREPKEPPPTTPHEYMLSLYRTL 174  
 Qy 121 TVTPKGQLPGGKAPPKAGSVSPSEFLKKAREPPPREPKPPPTTPHEYMLSLYRTL 180  
 Db 175 SDADRKGNSSVKLEAGLANITTSFIDKGQDDRGPAVVRKQRYVDFISALEKDGLLGAE 234  
 Qy 181 SDADRKGNSSVKLEAGLANITTSFIDKGQDDRGVPVVRKQRYVDFISALEKDGLLGAE 240  
 Db 235 ILRKKPLDVAPVPSGSRVAQLKSSCPGSRQPAALLDVRSVPLDGSNGVEFIDWKLF 294  
 Qy 241 ILRKKPSDTAKPAPGGGAAQLKSSCPGSRQPAALLDVRSVPLDGSNGVEFIDWKLF 300  
 Db 295 RNFNSAQLCLELEAWERGRAVDLRLGLGFERTARQVHEKALFLVFGRTKKRDLEFNEIKA 354  
 Qy 301 RNFNSAQLCLELEAWERGRAVDLRLGLGFDRAAQVHEKALFLVFGRTKKRDLEFNEIKA 360  
 Db 355 RSGQDDKTVYEYLFSSQRKRRAPLNATROGKRPKNLARCCKALHVNFKDMGDDWIIA 414  
 Qy 361 RSGQDDKTVYEYLFSSQRKRRAPLNATROGKRPKNLARCCKALHVNFKDMGDDWIIA 420  
 Db 415 PLEYEAFHCEGLCEFFPLRSHLEPTNHAIVQTLNMSMDPESTPPCCVPTRLSPISILFID 474  
 Qy 421 PLEYEAFHCEGLCEFFPLRSHLEPTNHAIVQTLNMSMDPESTPPCCVPTRLSPISILFID 480

Db 475 SANNVYKQEDVMVESCGR 495  
 QY 481 SANNVYKQEDVMVESCGR 501

RESULT 11  
 ID R40800 standard; Protein; 401 AA.

AC R40800;  
 DT 11-FEB-1994 (first entry)  
 DE TGF-beta-like clone MP-52 protein.  
 KW Human; transforming growth factor; beta; TGF-beta; pharmaceutical;  
 KW bone; cartilage; tooth; wound repair; immunosuppressor;  
 KW organ transplant; cosmetic surgery; antibody; diagnosis.  
 OS Homo sapiens.  
 PN W09316099-A.  
 PD 19-AUG-1993.  
 PF 12-FEB-1993; E00350.  
 PR 12-FEB-1992; EP-102324.  
 PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.  
 PI Hoesten G, Neidhardt H;  
 WPI: 93-272824/34.  
 N-PSDB: Q47709.

PT New transforming growth factor-beta family proteins and DNA -  
 used in tissue and wound repair, in treatment of bone, cartilage  
 and tooth defects, and antibodies for diagnosis  
 PS Claim 11; Page 19; 29pp; English.  
 CC The sequences given in R40800 and R45447 represent fragments of embryo  
 and liver derived human transforming growth factor-beta (TGF-beta)  
 respectively. The full length protein may be used in a pharmaceutical  
 composition for the treatment of various bone, cartilage or tooth  
 defects and in tissue and wound repair processes. These proteins may  
 also be used as immunosuppressors in organ transplants and in cosmetic  
 surgery. Antibodies raised against these proteins may be used for  
 diagnostic purposes.  
 SO Sequence 401 AA;

Query Match 79.9%; Score 2925; DB 1; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 2,39e-258;  
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 PGGPEPKGHPQTRQATARTVTPKGQPGKAPKAGSVSPSSFLKKAREPGPPREPKE 60  
 QY 101 PGGPEPKGHPQTRQATARTVTPKGQPGKAPKAGSVSPSSFLKKAREPGPPREPKE 160  
 Db 61 PFRPPPTPHEYMVLSYLTSLDADKRGKNSVSKLEAGLANITTSFIDKQDGRGPVVRKQ 120  
 QY 161 PFRPPPTPHEYMVLSYLTSLDADKRGKNSVSKLEAGLANITTSFIDKQDGRGPVVRKQ 220  
 Db 121 RYVFDISALEKDGGLGAEILRLKPKPSDTAKPAAPGGGAAQLKSSCPSGROPASLLDV 180  
 QY 221 RYVFDISALEKDGGLGAEILRLKPKPSDTAKPAAPGGGAAQLKSSCPSGROPASLLDV 280  
 Db 181 RSVPLDGGSGWEVFDIWLFRNFKNSAOLCLELEAWERGRAVDLRLGLGFDRAAROVHEKA 240  
 QY 281 RSVPLDGGSGWEVFDIWLFRNFKNSAOLCLELEAWERGRAVDLRLGLGFDRAAROVHEKA 340  
 Db 241 LFLVFGRTKKRDLFFNEIKARSGQDDKTVYELFSQRRKRRLATROGKRPKNLKARC 300  
 QY 341 LFLVFGRTKKRDLFFNEIKARSGQDDKTVYELFSQRRKRRLATROGKRPKNLKARC 400  
 Db 301 SRKALHVNFKMGWDWIIAPLEYEAFHCEGLCEPFLSHLEPTNHAIVTQTLNMSMDPES 360  
 QY 401 SRKALHVNFKMGWDWIIAPLEYEAFHCEGLCEPFLSHLEPTNHAIVTQTLNMSMDPES 460  
 Db 361 TPPTCCVTRLSPIILFIDSANNVYKQEDVMVESCGR 401  
 QY 461 TPPTCCVTRLSPIILFIDSANNVYKQEDVMVESCGR 501

RESULT 12  
 ID R95636 standard; Protein; 436 AA.  
 AC R95636;  
 DT 25-OCT-1996 (first entry)

DE Cartilage-derived morphogenetic protein-2.  
 KW Cattle; cartilage-derived morphogenetic protein-2; CDMP-2;  
 KW articular cartilage; chondrogenic; vulnery; implantation;  
 KW chondromalacia; osteoarthritis; therapy; joint repair.  
 OS Bos taurus.

FH Key Location/Qualifiers  
 FT region 1..312  
 FT /note= "Pro-region"  
 FT modified\_site 89..91  
 FT /note= "N-glycosylation site"  
 FT cleavage\_site 313..316  
 FT /note= "Proteolytic processing site"  
 FT domain 317..436  
 FT /note= "C-terminal mature domain"  
 FT peptide 352..382  
 FT /note= "Consensus conserved motif (R95641)"

PN W09614335-A1.  
 PD 17-MAY-1996.  
 PF 07-NOV-1994; U12814.  
 PR 07-NOV-1994; WO-U12814.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PI Chang SC, Luyten FP, Moos M;  
 DR WPI: 96-251714/25.  
 DR N-PSDB; T31602.  
 DR New purified cartilage extracts and proteins - used to stimulate the  
 development and repair of cartilage in vivo.  
 PS Claim 11; Fig 2; 34pp; English.

CC The sequence represents cattle articular cartilage-derived  
 morphogenetic protein-2 (CDMP-2). The N-terminal methionine and  
 signal peptide is missing, but part of the pro-region, a typical  
 proteolytic cleavage site and a C-terminal domain containing 7  
 highly conserved Cys residues characteristic of the transforming  
 growth factor-beta gene family are present. A single N-glycosylation  
 site is located in the pro-region. A consensus highly conserved  
 motif in CDMP proteins (R95641) is present in the C-terminal domain.  
 CC CDMP-2 is present in a purified cartilage extract (claimed) which  
 stimulates local cartilage formation and repair when combined with a  
 matrix and implanted in a mammal. The protein may be used in therapy  
 of e.g. chondromalacia or osteoarthritis, to heal joint surfaces, or  
 to repair cartilage after reconstructive surgery.  
 SO Sequence 436 AA;

Query Match 25.6%; Score 939; DB 1; Length 436;  
 Best Local Similarity 47.6%; Pred. No. 2,00e-72;  
 Matches 189; Conservative 85; Mismatches 69; Indels 54; Gaps 23;

Db 49 RRPQOQPEAREPPGRPLVPHEYMVLSYRTYSIAEKLGAINASFTQSSKANTITTSFVDR 108  
 QY 150 REPQPPREPKEP-FRPPPTTPHEYMVLSYRTLSADKRGKNSVSKLEAGLANITTSFIDK 208  
 Db 109 GLDDLSTPLRQKYLFDVSTLSKDEELVGADVRLFRQAPALA-P--PAAAPLAALRLP 165  
 QY 209 GODDRGPV-VRKQRYVFDISAL-EKDGGLGAEILRLKPKPSDTAKPAAPGGGAAQLKLS 266  
 Db 166 VAPAA---GSA-E-PPGAPAGPPGWEVFDVWGLRPP-QPWKOLCLELRAAWGEPGAED 219  
 QY 267 SCPSGRQFASLLDVRSPVGLDGSWEVFDIWLFRNFKNSAOLCLEL-EAW----- 316  
 Db 220 EARTPGQQPPPPDLRLSLGFGRRVTPQERALLVVFVSQRKTLFAEMREQLSATEVVG 279  
 QY 317 E-R--G--RAV--DLRGLGFDRAARQVHEKALFLVFGRTKKRDLF-----E-N--EKA 360  
 Db 280 PGGAGEGSGPPPPPPPPSGTTPDAGLWSPSPGRRRTAFASRHKRHKKSLRCSKRP 339  
 QY 361 RSG-QDDK-----TVY-EY-LFSQR--RKRRLAPLATROGKRPKNLKARC 404  
 Db 340 LHVNFKEKLGWDWIIAPLEYEAYHCEGVCDPFLRSHLEPTNHAIVTQTLNMSMDPSTPES 399  
 QY 405 LHVNFKEKMGWDWIIAPLEYEAFHCEGLCEPFLRSHLEPTNHAIVTQTLNMSMDPSTPPT 464  
 Db 400 CCVPTKLTPISTILYIDAGNNVYVNEYEMVVEGCGCR 436  
 QY 465 CCVPTKLTPISTILFIDSANNVYKQEDVMVVEGCGCR 501

RESULT 13  
 ID W26590 standard; Protein; 120 AA.  
 AC W26590;  
 DE Human MP52 protein.  
 KW Wound healing; tissue repair; tendonitis; carpal tunnel syndrome;  
 KW therapy.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Protein 1..120  
 FT Protein 19..120  
 FT Protein /note="Claim 5"  
 FT Protein /note="Claim 5"  
 PN US565882-A.  
 PD 19-AUG-1997.  
 PF 07-DEC-1993; 164103.  
 PR 22-DEC-1994; US-362670.  
 PR 07-DEC-1993; US-164103.  
 PR 25-MAR-1994; US-217780.  
 PR 02-NOV-1994; US-333576.  
 PA (GEM ) GENETICS INST INC.  
 PA (HARD ) HARVARD COLLEGE.  
 PI Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;  
 PI Wozney JM;  
 WT; 97-424270/39.  
 DR Inducing tendon and ligament formation using BMP-12, BMP-13 or MP-52  
 PT - useful for tissue healing and repair, treatment of tendonitis,  
 PT improving fixation of tendons to bone etc  
 PS Claim 5; Column 39-40; 43pp; English.  
 CC This polypeptide comprises human MP52. A claimed method for  
 CC inducing formation of tendon and/or ligament tissues involves the  
 CC administration of a composition containing at least one protein  
 CC selected from MP52, BMP-12 (see W26589) and BMP-13 (see W26591).  
 CC The method is used for tissue (including skin) healing and repair.  
 CC This is useful for treating tendonitis, carpal tunnel syndrome and  
 CC other defects of traumatic or congenital origin, in cosmetic  
 CC surgery and to improve fixation of tendons or ligaments to bone.  
 CC The specified proteins can also be used to increase activity of other  
 CC BMPs e.g. BMP-2 (see W26597).  
 SQ Sequence 120 AA;  
 Query Match 24.7%; Score 904; DB 1; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 3.33e-69;  
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 APLATROGKRPKSNLKCRCRKALHVNFKDGMGDDWIIAPLEYAFHCEGLCEPLRSHL 60  
 QY 382 APLATROGKRPKSNLKCRCRKALHVNFKDGMGDDWIIAPLEYAFHCEGLCEPLRSHL 441  
 Db 61 EPTNHAIVQTLNMSMDPEPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 120  
 QY 442 EPTNHAIVQTLNMSMDPEPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501  
 RESULT 14  
 ID W26590 standard; Protein; 120 AA.  
 AC W26590;  
 DE Human MP52 protein.  
 KW Wound healing; tissue repair; tendonitis; carpal tunnel syndrome;  
 KW therapy.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Protein 1..120  
 FT Protein 19..120  
 FT Protein /note="Claim 5"  
 FT Protein /note="Claim 5"  
 PN US565882-A.  
 PD 19-AUG-1997.  
 PF 07-DEC-1993; 164103.  
 PR 22-DEC-1994; US-362670.  
 PR 07-DEC-1993; US-164103.  
 PR 25-MAR-1994; US-217780.  
 PR 02-NOV-1994; US-333576.  
 PA (GEM ) GENETICS INST INC.  
 PA (HARD ) HARVARD COLLEGE.  
 PI Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;  
 PI Wozney JM;  
 WT; 97-424270/39.  
 DR Inducing tendon and ligament formation using BMP-12, BMP-13 or MP-52  
 PT - useful for tissue healing and repair, treatment of tendonitis,  
 PT improving fixation of tendons to bone etc  
 PS Claim 5; Column 39-40; 43pp; English.  
 CC This polypeptide comprises human MP52. A claimed method for  
 CC inducing formation of tendon and/or ligament tissues involves the  
 CC administration of a composition containing at least one protein  
 CC selected from MP52, BMP-12 (see W26589) and BMP-13 (see W26591).  
 CC The method is used for tissue (including skin) healing and repair.  
 CC This is useful for treating tendonitis, carpal tunnel syndrome and  
 CC other defects of traumatic or congenital origin, in cosmetic  
 CC surgery and to improve fixation of tendons or ligaments to bone.  
 CC The specified proteins can also be used to increase activity of other  
 CC BMPs e.g. BMP-2 (see W26597).  
 SQ Sequence 120 AA;  
 Query Match 24.7%; Score 904; DB 1; Length 120;  
 Best Local Similarity 100.0%; Pred. No. 3.33e-69;  
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 APLATROGKRPKSNLKCRCRKALHVNFKDGMGDDWIIAPLEYAFHCEGLCEPLRSHL 60  
 QY 382 APLATROGKRPKSNLKCRCRKALHVNFKDGMGDDWIIAPLEYAFHCEGLCEPLRSHL 441  
 Db 61 EPTNHAIVQTLNMSMDPEPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 120  
 QY 442 EPTNHAIVQTLNMSMDPEPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501  
 RESULT 15  
 ID W26591 standard; Protein; 321 AA.  
 AC W26591;  
 DT 21-JAN-1998 (first entry)  
 DE Human bone morphogenetic protein BMP-13.  
 KW BMP-13; bone morphogenetic protein; human; tendon; ligament;  
 KW wound healing; tissue repair; tendonitis; carpal tunnel syndrome;  
 KW therapy.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Peptide 1..201  
 FT Peptide /label="Sig\_peptide  
 FT Protein 202..321  
 FT Protein /label="Mat\_protein  
 FT Protein /note="Claim 5"  
 FT Protein 218..294  
 FT Protein /note="Claim 5"  
 PN US565882-A.  
 PD 19-AUG-1997.  
 PF 07-DEC-1993; 164103.  
 PR 22-DEC-1994; US-362670.  
 PR 07-DEC-1993; US-164103.  
 PR 25-MAR-1994; US-217780.  
 PR 02-NOV-1994; US-333576.  
 PA (GEM ) GENETICS INST INC.  
 PA (HARD ) HARVARD COLLEGE.  
 PI Celeste AJ, Melton DA, Rosen VA, Thomsen GH, Wolfman NM;  
 PI Wozney JM;  
 WT; 97-424270/39.  
 DR Inducing tendon and ligament formation using BMP-12, BMP-13 or MP-52  
 PT - useful for tissue healing and repair, treatment of tendonitis,  
 PT improving fixation of tendons to bone etc  
 PS Claim 5; Column 57-60; 43pp; English.  
 CC This polypeptide comprises a novel bone morphogenetic protein, its  
 CC designated BMP-13 that induces tendon and ligament formation. Its  
 CC amino acid sequence was deduced from isolated genomic clone vl-1  
 CC (see T90386). A claimed method for inducing formation of tendon  
 CC and/or ligament tissues involves the administration of a  
 CC composition containing at least one protein selected from BMP-13,  
 CC MP52 (see W26590) and BMP-12 (see W26589). The method is used for  
 CC tissue (including skin) healing and repair. This is useful for  
 CC treating tendonitis, carpal tunnel syndrome and other defects of  
 CC traumatic or congenital origin, in cosmetic surgery and to improve



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WQRFH (TM)

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Apr 19 19:44:13 2000; MasPar time 96.72 Seconds  
359.134 Million cell updates/sec  
Linear output not generated.

Title: >US-09-297-092-1  
Description: (1-501) from US09297092.pep  
Perfect Score: 3662  
Sequence: 1 MRLPKLLTFLWYLAWLDE.....ANNVYKQYEDWVSCGCR 501

Scoring table: PAM 150  
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: sptrembl12  
1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human  
5:sp.invertebrate 6:sp.mammal 7:sp.mnc 8:sp.organelle  
9:sp.phage 10:sp.plant 11:sp.rodent 12:sp.unclassified  
13:sp.vertebrate 14:sp.virus

Statistics: Mean 49.475; Variance 95.258; scale 0.519

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	2555	69.8	500	13	Q9W6G0 GDF-5 PROTEIN.	0.00e+00
2	2055	56.1	324	13	Q9XHW9 GROWTH DIFFERENTIATION	0.00e+00
3	1451	39.6	257	13	Q42303 GONATCT (FRAGMENT).	2.32e-276
4	1278	34.9	399	13	Q9W753 GROWTH AND DIFFERENTIA	1.07e-238
5	1200	32.8	412	13	Q12938 DYNAMO PROTEIN PRECURS	8.86e-222
6	822	22.4	126	13	Q93573 PUTATIVE GROWTH/DIFFER	1.45e-140
7	813	22.2	261	13	Q9W6C0 GROWTH/DIFFERENTIATION	1.19e-138
8	595	16.0	417	5	Q9XV07 BONE MORPHOGENETIC PRO	9.62e-91
9	553	15.1	204	5	Q9XZ69 BONE MORPHOGENETIC PRO	3.98e-84
10	551	15.0	191	5	Q28468 TRANSFORMING GROWTH FA	1.03e-83
11	551	15.0	411	13	Q93369 BONE MORPHOGENETIC PRO	1.03e-83
12	546	14.9	361	5	Q96504 BONE MORPHOGENETIC PRO	1.10e-82
13	545	14.9	453	13	BMP5.	1.77e-82
14	543	14.8	411	13	Q57573 BONE MORPHOGENETIC PRO	4.58e-82
15	536	14.6	178	5	Q25211 DECAPENTAPLEGIC (FRAGM	1.26e-80
16	534	14.6	400	13	Q57574 BONE GENETIC PROTEIN 4	3.25e-80
17	527	14.4	386	13	Q13109 BMP2.	8.92e-79
18	529	14.4	400	13	Q91703 PROTEIN 4.	3.46e-79
19	529	14.4	400	13	Q73818 BONE MORPHOGENETIC PRO	3.46e-79
20	526	14.4	424	13	Q9VGH7 OSTEOGENIC PROTEIN-1 H	1.43e-78

21	525	14.3	289	5	Q9XYQ8 BONE MORPHOGENETIC PRO	2.30e-78
22	521	14.2	400	13	BMP4.	1.52e-77
23	515	14.1	301	5	MGDF PRECURSOR.	2.58e-76
24	516	14.1	411	13	BMP2-4.	1.61e-76
25	509	13.9	313	13	BONE MORPHOGENETIC PRO	4.36e-75
26	509	13.9	614	5	DECAPENTAPLEGIC PROTEI	4.36e-75
27	505	13.8	373	13	Q98950 VGL.	2.87e-74
28	505	13.8	373	13	Q90723 GROWTH FACTOR CVGL.	2.87e-74
29	503	13.7	443	5	Q76851 HOMOLOG OF DPP SUBCLAS	7.35e-74
30	497	13.6	390	13	Q91597 ANTI-DORSALIZING MORPH	1.23e-72
31	491	13.4	67	6	Q02783 GROWTH DIFFERENTIATION	2.06e-71
32	483	13.2	421	11	Q921V8 BONE MORPHOGENETIC PRO	8.79e-70
33	478	13.1	354	13	Q9YGV1 DERRIERE.	9.13e-69
34	481	13.1	424	4	Q95393 BONE MORPHOGENETIC PRO	2.24e-69
35	476	13.0	365	5	Q02424 DECAPENTAPLEGIC PROTEI	2.33e-68
36	473	12.9	391	13	P87380 BONE MORPHOGENETIC PRO	9.47e-68
37	467	12.8	356	13	Q9YI39 VGL PROTEIN (FRAGMENT)	1.56e-66
38	467	12.8	365	5	Q76514 CET-1.	1.56e-66
39	463	12.6	428	5	O16134 TRANSFORMING GROWTH FA	1.01e-65
40	458	12.5	428	5	O16123 TRANSFORMING GROWTH FA	1.04e-64
41	452	12.3	683	5	Q94580 BONE MORPHOGENETIC PROTE	1.69e-63
42	447	12.2	428	11	Q9WV56 GROWTH/DIFFERENTIATION	1.73e-62
43	442	12.1	67	6	Q02784 GROWTH DIFFERENTIATION	1.76e-61
44	427	11.7	114	4	Q9Y571 GROWTH/DIFFERENTIATION	1.82e-58
45	421	11.5	99	13	O93254 DVR-1 (FRAGMENT).	2.90e-57

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	500 AA.
ID	Q9W6G0;			
AC	Q9W6G0;			
DT	01-NOV-1999 (Tremblrel. 12, Created)			
DT	01-NOV-1999 (Tremblrel. 12, Last sequence update)			
DT	01-NOV-1999 (Tremblrel. 12, Last annotation update)			
DE	GDF-5 PROTEIN.			
GN	GDF5.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;			
OC	Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 99146893.			
RA	FRANCIS-WEST P H., ABDELFAITAH A., CHEN P., ALLEN C., PARISH J.,			
RA	LAHER R., ALLEN S., MACPHERSON S., LUYTEN F.P., ARCHER C.W.;			
RT	"Mechanisms of Gdf-5 action during skeletal development."			
RL	Development 126:1305-1315(1999).			
CC	-1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.			
DR	EMBL: AF123389; AAD30451.1; -			
DR	PROSITE: PS00250; TGF_BETA; 1.			
KW	Glycoprotein.			
SQ	SEQUENCE 500 AA: 55952 MW; 743BA553 CRC32;			

Query Match	69.8%;	Score 2555;	DB 13;	Length 500;
Best Local Similarity	69.6%;	Pred. No. 0.00e+00;		
Matches	352;	Conservative	79;	Mismatches 64;
				Indels 11;
				Gaps 9;
Db	1	MKILHFLLLMHLWLSLDRVPGALSNSAQSNPGSKTDLLKAGKERTASRGAPR	60	
Qy	1	MRLPKLLTFLWYLAWLDEFTCVLGPDLGQRPQGRPLGAKAEKRPPLARN-VPR	59	
Db	61	AANHGFSTG-T-SKARAKSNAQAQALL-AKNDEQSVLSRTAVTEAKVGHLP-SRPSAV	116	
Qy	60	PGGHVGGGATNANARAKGGTQGTGLTQPKKDEPKLPPRPFGPEPKFHPPTQROATA	119	
Db	117	RTVTPKVNLSGKALKTKGTGTGTDASSFKTKTKTEPVTVQREAKETSPPTTPHEYMUS	176	
Qy	120	RTVTPGQLPGKAP-PRAGS--V-PSSFLAKAKREPPEKPEKFRPPPTTPHEYMUS	175	
Db	177	LYRTLSDAERKGVNSVKLEAGLANTITSFDKGDQERATIRKQKIFYDISALEKDGLL	236	
Qy	176	LYRTLSADARKGVNSVKLEAGLANTITSFDKGDQDRGPVVRKQRYVFDISALEKDGLL	235	

Db 237 VAEILRLKPNPDTWK--SHSSGKTSQVKLFSCSTNRQAATLLDSRTVSTIDTPKWEVFD 294  
 QY 236 GAEILRLKPNPDTAKPAAGGGRAAQKLSSCPGSRQPSALLDVRSPGLDGSWEVFD 295  
 Db 295 IWKLFERNKLVNLCFELETFDGRVADLRTVGFRNRTGROVNEKALFLVGRKKRDLFF 354  
 QY 296 IWKLFERNKLVNLCFELETFDGRVADLRTVGFRNRTGROVNEKALFLVGRKKRDLFF 355  
 Db 355 NEIKARSGDDKTYEYLFNORRRRRAPLATROGKRPSKNLKPCCSRKALHVNFKMGWD 414  
 QY 356 NEIKARSGDDKTYEYLFNORRRRRAPLATROGKRPSKNLKPCCSRKALHVNFKMGWD 415  
 Db 415 DWIIAPLEYEYHCEGLCEFPRLSHLEPTNHAVIQTLMNSMDPESTPTCCVPTRLSPIS 474  
 QY 416 DWIIAPLEYEYHCEGLCEFPRLSHLEPTNHAVIQTLMNSMDPESTPTCCVPTRLSPIS 475  
 Db 475 ILFTDSANNVVKQYEDMVVESCGR 500  
 QY 476 ILFTDSANNVVKQYEDMVVESCGR 501

RESULT 2  
 ID QYHW9 PRELIMINARY; PRT; 324 AA.  
 AC QYHW9;  
 DT 01-MAY-1999 (Tremblrel. 10, Created)  
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)  
 DE GROWTH DIFFERENTIATION FACTOR 5 PRECURSOR (FRAGMENT).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;  
 OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-LEG BUD;  
 RX MEDLINE; 99119368.  
 RA MERINO R., MACIAS D., GANAN Y., ECONOMIDES A.N., WANG X., WU Q.,  
 RA STAHL N., SAMPATH K.T., VARONA P., HURLE J.M.;  
 RT "Expression and function of Gdf-5 during digit skeletogenesis in the  
 RT embryonic chick leg bud";  
 RL Dev. Biol. 206:33-45(1999).  
 CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.  
 DR EMBL; AF075441; AAD14568.1;  
 DR HSSP; P18075; IBMP.  
 DR PROSITE; PS00250; TGF\_BETA; 1.  
 KW Glycoprotein.  
 FT NON\_TER 1 1  
 FT CHAIN 324 324  
 FT SEQUENCE 324 AA; 37206 MW; E2CF56AC CRC32;

Query Match 56.1%; Score 2055; DB 13; Length 324;  
 Best Local Similarity 83.7%; Pred. No. 0.00e+00; Mismatches 17; Indels 2; Gaps 1;  
 Matches 273; Conservative 34;  
 Db 1 ITPHEYMLSYRTLSDAERKGVNSVKLEAGLNTIISFDKGDERTAPTRKOKYLFDI 60  
 QY 167 ITPHEYMLSYRTLSDAERKGVNSVKLEAGLNTIISFDKGDERTAPTRKOKYLFDI 226  
 Db 61 SALEKDGLLGAEILRLKPNPDTWK--SHSSGKTSQVKLFSCSTNRQAATLLDSRTVST 118  
 QY 227 SALEKDGLLGAEILRLKPNPDTWK--SHSSGKTSQVKLFSCSTNRQAATLLDSRTVST 286  
 Db 119 DTPKWEVFDIWKLFERNKLVNLCFELETFDGRVADLRTVGFRNRTGROVNEKALFLVFG 178  
 QY 287 DGSWEVFDIWKLFERNKLVNLCFELETFDGRVADLRTVGFRNRTGROVNEKALFLVFG 346  
 Db 179 RTKKRDLFFNEIKARSGDDKTYEYLFNORRRRRAPLATROGKRPSKNLKPCCSRKALH 238  
 QY 347 RTKKRDLFFNEIKARSGDDKTYEYLFNORRRRRAPLATROGKRPSKNLKPCCSRKALH 406  
 Db 239 VNFKMGWDWIIAPLEYEYHCEGLCEFPRLSHLEPTNHAVIQTLMNSMDPESTPTCC 298  
 QY 407 VNFKMGWDWIIAPLEYEYHCEGLCEFPRLSHLEPTNHAVIQTLMNSMDPESTPTCC 466

Db 299 VPTRLSPISILFIDSANNVVKQYEE 324  
 QY 467 VPTRLSPISILFIDSANNVVKQYED 492  
 RESULT 3  
 ID Q42303 PRELIMINARY; PRT; 257 AA.  
 AC Q42303;  
 DT 01-JAN-1998 (Tremblrel. 05, Created)  
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)  
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)  
 DE CONTACT (FRAGMENT).  
 GN CONTACT.  
 OS Brachydanio rerio (Zebrafish) (Zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
 OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Cyprininae; Rasbora; Rasbora; Danio.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 97398455.  
 RA BRUNEAU S., MOURRAIN P., ROSA F.M.;  
 RT "Expression of contact, a new zebrafish DVR member, marks mesenchymal  
 RT cell lineages in the developing pectoral fins and head and is  
 RT regulated by retinoic acid";  
 RL Mech. Dev. 65:163-173(1997).  
 CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.  
 DR EMBL; Y12005; CAA72733.1;  
 DR HSSP; P18075; IBMP.  
 DR ZFIN; ZDB-GENE-990415-39; contact.  
 DR PROSITE; PS00250; TGF\_BETA; 1.  
 DR PRAM; PF00019; TGF-beta; 1.  
 KW Glycoprotein.  
 FT NON\_TER 1 1  
 FT CHAIN 140 257  
 FT SEQUENCE 257 AA; 29787 MW; 6BDDCADC CRC32;  
 Query Match 39.6%; Score 1451; DB 13; Length 257;  
 Best Local Similarity 72.4%; Pred. No. 2.32e-276;  
 Matches 189; Conservative 41; Mismatches 27; Indels 4; Gaps 4;  
 Db 1 ILRKKHMSRK-ATFSEGMAV-LRLFTCASGKNAVILQARPPDSHSASVWEVDIWKVF 58  
 QY 241 ILRKKPSDTAKPAAGGGRAAQKLSSCPGSRQPSALLDVRSPGLDGSWEVFDIWKLF 300  
 Db 59 KNFANTPOLCLELDVADHDGRLDLRLILGLSRAGRTKEKAFVVFGRKKRGLFNEIKA 118  
 QY 301 RNFKNSAQLCLELEAWERGRAVDLRLGLFDRARQVHEKALFLVFGRTKKRDLFFNEIKA 360  
 Db 119 RSGHNDKTVYELFTQRRMRAPLP-R-GKKPIKNKQRCNRKOLHVNFKMGWDWIIA 176  
 QY 361 RSGODDKTVYELFVSQRRKRAPLATROGKRPSKNLKPCCSRKALHVNFKMGWDWIIA 420  
 Db 177 PLEYEAFHCEGLCEFPRLSHLEPTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFID 236  
 QY 421 PLEYEAFHCEGLCEFPRLSHLEPTNHAVIQTLMNSMDPESTPTCCVPTRLSPISILFID 480  
 Db 237 SANNVVKQYEDMVVESCGR 257  
 QY 481 SANNVVKQYEDMVVESCGR 501  
 RESULT 4  
 ID Q9W753 PRELIMINARY; PRT; 399 AA.  
 AC Q9W753;  
 DT 01-NOV-1999 (Tremblrel. 12, Created)  
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)  
 DE GROWTH AND DIFFERENTIATION FACTOR 6.  
 GN GDF6.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;  
 OC Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae;  
 OC Xenopus.



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RN  SEQUENCE FROM N.A.
RA  CHANG C., HEMWATI-BRIVANLOU A.;
RT  "Xenopus GDF6, a new antagonist of noggin and a partner of BMPs.";
RL  Development 0:0-0(1999).
CC  -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR  EMBL; AF15125; AAD38402.1;
DR  PROSITE; PS00250; TGF_BETA; 1.
KW  Glycoprotein.
SQ  SEQUENCE 399 AA; 45571 MW; 98A43227 CRC32;

Query Match      34.9%; Score 1278; DB 13; Length 399;
Best Local Similarity 52.0%; Pred. No. 1.07e-238;
Matches 180; Conservative 85; Mismatches 63; Indels 18; Gaps 14;

Db  63 PAVPHEVMSLYTFTFAEKLGINASFFQSSKSNANTISSFVDRRNLSPSLKRKYL 122
Qy  165 PPTPHEVMSLYRTLSADRRKGNSSVKLEAGLANTITSFDKQDDRG-PVVRKQRYV 223
Db  123 FDSVLSDEELVGAELRVFKAPVESAK--TPLD--LYNLQVTSCTSOAQLDYRTLDR 178
224 FDISAL-EKDGLLGAELRIILKKSDTAKPAAPGGGAAQLKLSCPSGROPA-SLLDVR 281
Db  179 DTFS---PGQVDFVWKSLODQCKQICVELKAISITTTGLEVNLRLSLGAKRPSRHOE 235
Qy  282 SVPGLDGSGWEVFDIWKLFNRKNSA-QLCLELEA-W-ERGRAVDLRLGLGFDRAARQVHE 338
Db  236 KALLVVFTKSRKNLY-NELKEQV-HSSKSMEKEARLHKTRRRRTTFNSRHGKRGRK 293
Qy  339 KALFLVFGRTKKRD-LFFNEI-KARSGQDDKTVY-EY-L-FSQRRKRRLATYRQGRPSKN 395
Db  294 SRLRCSKPLHVNFKELGWDDWIAPLEYEAHCEGVCDFPLRSHLEPTNHAIQTLMN 353
Qy  396 LKARCSKALHVNFKMGWDWIAPLEYEAFHCEGLCEFFPLRSHLEPTNHAIQTLMN 455
Db  354 MNPSTPPSCVPTKLTPIISILYIDAGNNVYKQYEDMVVESCGR 399
Qy  456 MDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501

RESULT 5
ID  012938 PRELIMINARY; PRT; 412 AA.
AC  012938;
DT  01-JUL-1997 (TrEMBLrel. 04, Created)
DT  01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DE  01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE  DYNAMO PROTEIN PRECURSOR.
GN  DYNAMO.
OC  Brachydanio rerio (Zebrafish) (Zebra danio).
OS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC  Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC  Cyprinidae; Cyprininae; Rasbora; Danio.
RN  SEQUENCE FROM N.A.
RA  BRUNEAU S., ROSA F.;
RT  "Dynamo, a new zebrafish DVR member of the TGF-beta superfamily is
RT  expressed in the posterior neural tube and is up-regulated by Sonic
RT  hedgehog.";
RL  Mech. Dev. 61:199-212(1997).
CC  -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR  EMBL; X99769; CAA68102.1;
DR  HSP; P18075; 1BMP.
DR  ZFIN; ZDB-GENE-980526-442; dynamo.
DR  PROSITE; PS00250; TGF_beta; 1.
DR  PFAM; PF00019; TGF_beta; 1.
DR  PFAM; PF00688; TGF_beta_propeptide; 1.
DR  PRINTS; PR00438; GFCYSKNOF.
KW  Signal; Glycoprotein.
FT  SIGNAL 1 17 POTENTIAL.
FT  CHAIN 293 412 DYNAMO PROTEIN.
SQ  SEQUENCE 412 AA; 47071 MW; 1E5AE13 CRC32;

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Query Match      32.8%; Score 1200; DB 13; Length 412;
Best Local Similarity 50.7%; Pred. No. 8.86e-222;
Matches 176; Conservative 75; Mismatches 79; Indels 17; Gaps 16;

Db  72 AIEPHDMISYKTFSAAEKLGNASFFRSKKAANTITSFVDEGDDHNSPLMRQKYL 131
Qy  166 PITPHEVMSLYRTLSADRRKGNSSVKLEAGLANTITSFDKQDDRG-PVVRKQRYV 224
Db  132 DVSTLSENVEILGAELRIY-TKISGSFRASSETGPV-EIQL-LS-CQSHVLDSDQ-TL-DL 185
Qy  225 DISAL-EKDGLLGAELRIILKKSDTAKPAAPGGGAAQLKLSCPSGROPA-SLLDVR 283
Db  186 EDAHKPKVEVDFVWEIPEKROHSHGNFCLERLATLNPEDIDLOVLGFRHGRGPOLK 245
Qy  284 PGLDGSHEVEDIWKLF--R-NFKNSAQLCLEL-EAWER-GRAVDLRLGLGFDRAARQVHE 338
Db  246 KAILVVFTRSKKROSLFYEKREKIKLWGLDSIGKERRSHSKTRRSRRRTALPNRHGKRHK 305
Qy  339 KALFLVFGRTKKRD-LFFNEI-KAR-SGQDDKTVYELFSQ-RRKRRAPLATYRQGRPSK 394
Db  306 KSKRCSKPLHVNFKELGWDDWIAPLDYEAHCEGVCDFPLRSHLEPTNHAIQTLMN 365
Qy  395 NLKARCSKALHVNFKMGWDWIAPLEYEAFHCEGLCEFFPLRSHLEPTNHAIQTLMN 454
Db  366 SMNPSNMPPSCVPSKLTPIISILYIDAGNNVYKQYEDMVVESCGR 412
Qy  455 SMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501

RESULT 6
ID  093573 PRELIMINARY; PRT; 126 AA.
AC  093573;
DT  01-NOV-1998 (TrEMBLrel. 08, Created)
DT  01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE  01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE  PUTATIVE GROWTH/DIFFERENTIATION FACTOR 6/7 (FRAGMENT).
GN  GDF6/7.
OS  Gallus gallus (Chicken).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC  Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN  SEQUENCE FROM N.A.
RA  LEE K.J., MENDELSON M., JESSELL T.M.;
RT  "Neuronal patterning by BMPs: A requirement for GDF7 in the generation
RT  of a discrete class of commissural interneurons in the mouse spinal
RT  cord.";
RL  Genes Dev. 0:0-0(1998).
CC  -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR  EMBL; AF089086; AAC97113.1;
DR  HSP; P18075; 1BMP.
DR  PROSITE; PS00250; TGF_beta; 1.
DR  PFAM; PF00019; TGF_beta; 1.
KW  Glycoprotein.
FT  NON_TER 1 1
FT  SEQUENCE 126 AA; 14265 MW; 612DD07 CRC32;

Query Match      22.4%; Score 822; DB 13; Length 126;
Best Local Similarity 79.4%; Pred. No. 1.45e-140;
Matches 100; Conservative 20; Mismatches 5; Indels 1; Gaps 1;

Db  1 RKRRTTAAARSGGRGHGKAKTRCSRAKPLHVNFKELGWDDWIAPLDYEAHCEGVCDF 60
Qy  377 RKRRLAPLATYRQGR-PSKNLKAARCSKALHVNFKMGWDWIAPLEYEAFHCEGLCEFF 435
Db  61 PLRSHLEPTNHAIQTLMNSMDPESTPPSCVPSKLTPIISILYIDAGNNVYKQYEDMVV 120
Qy  436 PLRSHLEPTNHAIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVV 495
Db  121 ETCGCR 126
FT  SIGNAL 1 17
FT  CHAIN 293 412 DYNAMO PROTEIN.
SQ  SEQUENCE 412 AA; 47071 MW; 1E5AE13 CRC32;

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RESULT 7
ID Q9W6C0 PRELIMINARY; PRT; 261 AA.
AC Q9W6C0;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 7 (FRAGMENT).
GN GDF7.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprininae; Rasboreinae; Danio.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99148135.
RA DAVIDSON A.J., POSTLETHWAIT J.H., YAN Y.L., BEIER D.R., VAN DOREN C.,
RA FERNANDEZ D., CELESTE A.J., CROSIER K.E., CROSIER P.S.;
RA "Isolation of zebrafish gdf7 and comparative genetic mapping of genes
RA belonging to the growth/differentiation factor 5, 6, 7 subgroup of the
RA TGF-beta superfamily.";
RL Genome Res. 9:121-129(1999).
CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; AF113023; AAD20829.1; -.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Glycoprotein.
FT NON_TER
SQ SEQUENCE 261 AA; 29414 MW; 82E59637 CRC32;

Query Match 22.2%; Score 813; DB 13; Length 261;
Best Local Similarity 55.9%; Pred. No. 1.19e+38;
Matches 124; Conservative 41; Mismatches 39; Indels 18; Gaps 12;

Db 40 KQHTAEDTRLLCLLSISAVSDNNEAVHPGMLGSLRSDQDQTHRALIVASQARRKENLF 99
QY 298 KLFNFNKSQAQLCELEA-WERGRAVDLRG-LGFDRAARQVHEKALFLVFGTKKRD-LF 354
Db 100 REIREKIRAMKRFNPTPHSKTGHPHRRRRRTLAGRGVGPITTSKGKGGRRRTR 159
QY 355 --FNE-IKASGQD-DKTVVEY-L--FS-QRRKRRAPLATQGRK--S--KN---UKAR 399
Db 160 CSRKPLHVNFKELGWDWIIAPLDYEAHCEGLCDFPLRSHLEPTNHAIIQTLNMSDPE 219
QY 400 CSRKALHVNFKDGMWDWIIAPLEAFAHCEGLCEFLRSHLEPTNHAIVQTLNMSDPE 459
Db 220 STPSCCVPSKLSIPISILYIDSGNNVYKQYEDMVVESCGR 261
QY 460 STPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501

RESULT 8
ID Q9XQ7 PRELIMINARY; PRT; 417 AA.
AC Q9XQ7;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN BMP2/4.
GN BMP2/4.
OS Lytechinus variegatus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
OC Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae; Lytechinus.
RN [1]
RP SEQUENCE FROM N.A.
RA ANGERER L.M., OLEKSYN D.W., LOGAN C.Y., MCCLAY D.R., DALE L.,
RA ANGERER R.C.;
RA "A BMP pathway regulates cell fate allocation along the sea urchin
RA animal-vegetal embryonic axis.";
RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; AF119712; AAD28038.1; -.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Glycoprotein.
SQ SEQUENCE 417 AA; 47727 MW; AE44D1A9 CRC32;

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Query Match 16.0%; Score 585; DB 5; Length 417;
Best Local Similarity 32.1%; Pred. No. 9.62e-91;
Matches 114; Conservative 82; Mismatches 142; Indels 17; Gaps 17;

Db 68 KERPRQGLRVFOYMDLYRSHTHQDGSIMHFDHLSGTGTANTIRSYHHEDAGQVLP 127
QY 159 KEPRPPP-ITPHEYMLSLYTLSD-ADKGGNSSVK-LEAGLANTITTSFDKGDDGRGP 215
Db 128 TEHRHTVINISITMPABEVLITMAELRFLKDLDEHSIAKRHALDDRRKSLPIHYMORIN 187
QY 216 VVR-KQRYVEDISALEKDGGLG-AELRLRKPSD-T-AKPAAPGGRAAQ-LK-LSSCP 269
Db 188 VFHLKPVARNRDTIKRLIDRLVDNRSSWESP-DYRPAVTSWVVEPKNHGLEIIDL 245
QY 270 SGROPASLLDVR-SVPGLDGSGW-EVFDI-WKLFNFKNSAQLCELEAWERGRAVDLRG 326
Db 247 -SRGRPSNNHHVRVTREADPSKVQELQ-NEEDERWFQTRPOIVTY-SDGRTKRSP-SS 302
QY 327 LGFDRAARQVHEKALFLVFGTKKRDLFNEIKARSGDDKTVVEYLFSPQRKRPLAT 386
Db 303 RGRKRRKRLKANCRRHPLYVDFSDVHNDWIVAPAGYQAYYCHGECFPPLAEHLNTNH 362
QY 387 RQGRKPSKNLKCRCRKALHVNFKDGMWDWIIAPLEAFAHCEGLCEFLRSHLEPTNH 446
Db 363 AIYQTLVNSVPALVPKACCGPTLSAISMLYLDYEYKVLKNYQDMVVEGCGCR 417
QY 447 AVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501

RESULT 9
ID Q9XZ69 PRELIMINARY; PRT; 204 AA.
AC Q9XZ69;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2/4 HOMOLOG (FRAGMENT).
GN BMP2/4.
OS Tripneustes gratilla (Hawaiian sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
OC Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae; Tripneustes.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99262121.
RA HWANG S.-P.L., CHEN C.A., CHEN C.-P.;
RA "Sea urchin TgBMP2/4 gene encoding a bone morphogenetic protein
RA closely related to vertebrate BMP2 and BMP4 with maximal expression at
RA the later stages of embryonic development.";
RA Biochem. Biophys. Res. Commun. 258:457-463(1999).
CC -1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; AF133305; AAD30538.1; -.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Glycoprotein.
FT NON_TER
SQ SEQUENCE 204 AA; 23697 MW; A0988AC4 CRC32;

Query Match 15.1%; Score 553; DB 5; Length 204;
Best Local Similarity 53.2%; Pred. No. 3.98e-84;
Matches 66; Conservative 27; Mismatches 31; Indels 0; Gaps 0;

Db 81 RTRKSTSSRSRRKRLKANCRRHPLYVDFSDVHNDWIVAPAGYQAYYCHGECFPPL 140
QY 378 RKRAPLATQGRKPSKNLKCRCRKALHVNFKDGMWDWIIAPLEAFAHCEGLCEFL 437
Db 141 AEHLNTNHAIVQTLVNSVPALVPKACCVPTLSAISMLYLDYEYKVLKNYQDMVVEG 200
QY 438 RSHLEPTNHAIVQTLNMSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVE 497
Db 201 CGCR 204
QY 498 CGCR 501

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RESULT 10
ID Q26468; PRELIMINARY; PRT; 191 AA.
AC Q26468;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE TRANSFORMING GROWTH FACTOR-BETA (FRAGMENT).
OS Schistocerca americana (American grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Acridomorpha; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorphia; Acridoidea; Acrididae; Cyrtacanthacridinae;
OC Schistocerca.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95395871.
RA NEWFIELD S.J., GELBART W.M.;
RT "Identification of two Drosophila TGF-beta family members in the
RT grasshopper Schistocerca americana."
RN J. Mol. Evol. 41:155-160(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87090408.
RA PADGETT R.W., JOHNSTON R.D., GELBART W.M.;
RT "A transcript from a Drosophila pattern gene predicts a protein
RT homologous to the transforming growth factor-beta family."
RN Nature 325:81-84(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89072730.
RA WOZNEY J.M., ROSEN V., CELESTE A.J., MITSOCK L.M., WHITTERS M.J.,
RA KRIZ R.W., HEWICK R.M., WANG E.A.;
RT "Novel regulators of bone formation: molecular clones and
RT activities."
RN Science 242:1528-1534(1988).
CC -I- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; U23785; AAA81169.1; -.
DR HSSP; P18075; 1BMP.
DR PROSITE; PS00250; TGF-BETA; 1.
DR PFAM; PF00019; TGF-beta; 1.
KW Glycoprotein.
KW NON-TER
SQ SEQUENCE 191 AA; 21879 MW; ED3D3318 CRC32;

Query Match 15.0%; Score 551; DB 5; Length 191;
Best Local Similarity 50.0%; Pred. No. 1.03e-83;
Matches 64; Conservative 34; Mismatches 27; Indels 3; Gaps 2;

Db 66 PQRRKNGAPPSSRSKR--KDQSTCRRHPLYVDREVGDWDWIAPPGYEGWYCHGDC 123
:||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
375 SQRR-KRAPLATROGKRPSKALKARCSKALHVNFKDGMGDDWIIAPLEYAFHCEGLC 433
:||||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 124 PPPLSAHNNSTNHAVOTLMNSMPLGPKACIPTQTSTISMLYLBESKVLKNYHEM 183
||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 434 EPLRSLEPTNHAIVQTLNMSMDPESTPPTCCVPTRLSPISILFIDSANNVYKQYEDM 493
:||||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 184 AVVCGCR 191
I :|||||
QY 494 VVESCGR 501

RESULT 11
ID O93369; PRELIMINARY; PRT; 411 AA.
AC O93369;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2.
CN BMP2.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Rasbora; Danio.
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-FW;
RX MEDLINE; 97231284.
RA NIKAI DO M., TADA M., SAI T., UENO N.;
RT "Conservation of BMP signaling in zebrafish mesoderm patterning."
RL Mech. Dev. 61:73-88(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-FW;
RX MEDLINE; 98072322.
RA KISHIMOTO Y., LEE K.H., ZON L., HAMMERSCHMIDT M., SCHULTE-MERKER S.;
RT "The molecular nature of zebrafish swirl: BMP2 function is essential
RT during early dorsoventral patterning."
RL Development 124:4457-4466(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-FW;
RA LEE K.H., MARDEN J.J., THOMPSON M.S., MACLENNAN H., KISHIMOTO Y.,
RA PRATT S.J., SCHULTE-MERKER S., HAMMERSCHMIDT M., JOHNSON S.L.,
RA POSTLETHWAITE J.H., BEIER D.C., ZON L.I.;
RT "Cloning and Genetic Mapping of Zebrafish BMP-2."
RL Dev. Genet. 23:0-0(1998).
CC -I- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
DR EMBL; AF072456; AAC25595.1; -.
DR HSSP; P18075; 1BMP.
DR PROSITE; PS00250; TGF-BETA; 1.
DR PFAM; PF00019; TGF-beta; 1.
DR PFAM; PF00688; TGF-beta-propeptide; 1.
KW Glycoprotein.
SQ SEQUENCE 411 AA; 46873 MW; AF0342A5 CRC32;

Query Match 15.0%; Score 551; DB 13; Length 411;
Best Local Similarity 32.2%; Pred. No. 1.03e-83;
Matches 117; Conservative 98; Mismatches 116; Indels 32; Gaps 28;

Db 64 RKPT-PSKSA-VVPO-YMLDLYMHSENDPPNRRPRSTMGKHVRAASRANTIRSFHHE 120
:||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 156 REPKEPPPPPTTPEYMLSLY--RTLS-D-AD-RKGGNSSVK-LE--AGLANTITSFI-D 207
:||||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 121 EAFEALSLKGTTOQFFNLTSIPGELISAEELRIPRDQVLGDASTSGFHRINIEVF 180
:||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 208 KGQDDRGFV-VRK-QRYVFDISALEKDGILLGA-ELRILRKRP-SDTAKPAAPGCGRAAQL 263
:||||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 181 RPALAPS-KEPLTRLLDTRLVODSHTR-WESFDVGSAVARWARESOHNHGLLVEYL-HPK 237
:||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 264 KLSSCPSPGRQP-ASLLDVRSPVGLDGSWEVEDI-WKLFNFKNSAQLC-LELEAWERGR 320
:||||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 238 ESEVESEAESENRRKHVRVSRSLHADEDSWAQARPLLVT-Y-SHDGQG-TAV---LHNSRE 291
:||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 321 AVDLRGLGFDRAARQVH-EKALFL-VFGTKKRDLEFNEIKARSGQDDKTVEYLFSSQR 378
:||||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 292 KQARRGQKP-RR-KHORSNRRHALYVDFSDVGWNEWIVAPPYHAFYCHGECPPPLP 349
:||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 379 KRRAPLATROGKRPSKALKARCSKALHVNFKDGMGDDWIIAPLEYAFHCEGLCEFLR 438
:||||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 350 DHLNSTNHAIVQTLNMSVNSN-IPKACCIPTLSLILYLBESKVLKNYQDMVVECC 408
:||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 439 SHLEPTNHAIVQTLNMSMDPESTPPTCCVPTRLSPISILFIDSANNVYKQYEDM 498
:||||| : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 409 GCR 411
|||||
QY 499 GCR 501

RESULT 12
ID O96504; PRELIMINARY; PRT; 361 AA.
AC O96504;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2/4.
GN AMPHIBMP2/4.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).

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RESULT 15
ID Q25211 PRELIMINARY: PRT: 178 AA.
AC Q25211
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE DECAPENTAPLEGIC (FRAGMENT).
OS Junonia coenia (Peacock butterfly) (Precis coenia).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Nymphalinae; Junonia.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-WHOLE ANIMAL;
EX MEDLINE; 94287189.
RA CARROLL S.B., GATES J., KEYS D.N., PADDOCK S.W., PANGANIBAN G.E.,
RA SELEGUE J.E., WILLIAMS J.A.;
RT "Pattern formation and eyespot determination in butterfly wings.";
RL Science 265:109-114(1994).
-1- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
EMBL; L42141; ABA46367.1; -.
DR HSP; P18075; IEMP.
DR PROSITE; PS00250; TGF_BETA; 1.
DR PFAM; PF00019; TGF-beta; 1.
KW Glycoprotein.
FT NON_TER
SQ SEQUENCE 178 AA; 20443 MW; C41C9523 CRC32;

Query Match 14.6%; Score 536; DB 5; Length 178;
Best Local Similarity 50.4%; Pred. No. 1.26e-80;
Matches 63; Conservative 30; Mismatches 32; Indels 0; Gaps 0;

Db 54 RNKRAQRKGRHRRHRRKEAREICORRPLFVDFAVGSWDIVAPHGDAYYCQGDCEFP 113
Qy | | | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
377 RRRKRAPLATRQGRKPSKRLKARCSKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFP 436

Db 114 LSDHLNGTNGHAIQVTLVNSVNPAAVPKACCVPTQLSSISMLYMDENVNVLKNYQDMVV 173
Qy | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
437 LRSHLEPTNHAVIQTLNMSMDPESTPPTCCVPTRLSPISILFIDSANNVYKQYEDMYVE 496

Db 174 GCGCR 178
Qy : | | | |

Qy 497 SCGR 501
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Search completed: Wed Apr 19 19:48:43 2000  
Job time : 270 secs.

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msrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Wed Apr 19 19:41:59 2000; Maspar time 36.54 Seconds
409.433 Million cell updates/sec
Cellar output not generated.

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```
>US-09-297-092-1
Title:
Description: (1-501) from US09297092.pap
Perfect Score: 3662
Sequence: 1 MRPLKLLTFLWYLAWLDE.....ANNVYKQYEDMNVESGGR 501
```

Searched: 82229 seqs, 29864866 residues

```
Database: swiss-prot38
          1:swissprot
```

Statistics: Mean 50.721; Variance 91.436; scale 0.555

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Query			DB	ID	Description	Pred. No.
	Score	Match	Length				
1	3608	98.5	501	1	GDF5_HUMAN	GROWTH/DIFFERENTIATION	0.00e+00
2	3332	91.0	495	1	GDF5_MOUSE	GROWTH/DIFFERENTIATION	0.00e+00
3	939	25.6	436	1	GDF6_BOVIN	GROWTH/DIFFERENTIATION	1.63e-170
4	832	22.7	125	1	GDF6_MOUSE	GROWTH/DIFFERENTIATION	3.69e-15
5	735	20.1	151	1	GDF7_MOUSE	GROWTH/DIFFERENTIATION	3.01e-13
6	566	15.5	405	1	BMP4_CHICK	BONE MORPHOGENETIC PRO	1.32e-92
7	565	15.4	396	1	BMP2_DAMIA	BONE MORPHOGENETIC PRO	2.20e-92
8	544	14.9	393	1	BMP2_RAT	BONE MORPHOGENETIC PRO	9.04e-88
9	544	14.9	395	1	BMP2_RABIT	BONE MORPHOGENETIC PRO	9.04e-88
10	546	14.9	396	1	BMP2_HUMAN	BONE MORPHOGENETIC PRO	3.29e-88
11	545	14.9	398	1	BMP4_XENLA	BONE MORPHOGENETIC PRO	5.46e-88
12	546	14.9	452	1	BMP5_MOUSE	BONE MORPHOGENETIC PRO	3.29e-88
13	543	14.8	454	1	BMP5_HUMAN	BONE MORPHOGENETIC PRO	1.50e-87
14	533	14.6	394	1	BMP2_MOUSE	BONE MORPHOGENETIC PRO	2.33e-85
15	536	14.6	398	1	BMPB_XENLA	BONE MORPHOGENETIC PRO	5.12e-86
16	533	14.6	408	1	BMP4_HUMAN	BONE MORPHOGENETIC PRO	2.33e-85
17	531	14.5	372	1	DECA_TRICA	DECAPENTAPLEGIC PROEI	6.37e-85
18	532	14.5	408	1	BMP4_DAMIA	BONE MORPHOGENETIC PRO	3.85e-85
19	530	14.5	408	1	BMP4_MOUSE	BONE MORPHOGENETIC PRO	1.05e-84
20	530	14.5	408	1	BMP4_RAT	BONE MORPHOGENETIC PRO	1.05e-84
21	529	14.4	401	1	BMP4_XENLA	BONE MORPHOGENETIC PRO	1.74e-84
22	529	14.4	409	1	BMP4_RABIT	BONE MORPHOGENETIC PRO	1.74e-84
23	523	14.3	383	1	UNIV_STRPU	UNIVIN PRECURSOR.	3.57e-83

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CC -----  
 DR EMBL; X80915; CAA56874.1; -;  
 DR EMBL; U13660; AAA57007.1; -;  
 DR HSSP; U13660; IBMP.  
 DR MIM; 601146; -;  
 DR MIM; 201250; -;  
 DR MIM; 200700; -;  
 DR PROSITE; PS00250; TGF\_BETA; 1.  
 DR PFAM; PF00019; TGF-beta; 1.  
 DR PFAM; PF00688; TGF-beta; 1.  
 DR KW Signal; Growth factor; Cytokine; Glycoprotein.  
 DR KW Signal; Growth factor; Cytokine; Glycoprotein.  
 FT SIGNAL 1 ? POTENTIAL.  
 FT PROPEP ? 381 POTENTIAL.  
 FT CHAIN 382 501 POTENTIAL.  
 FT CHAIN 382 501 POTENTIAL.  
 FT DISULFID 400 466 GROWTH/DIFFERENTIATION FACTOR 5.  
 FT DISULFID 429 498 BY SIMILARITY.  
 FT DISULFID 433 500 BY SIMILARITY.  
 FT DISULFID 465 465 BY SIMILARITY.  
 FT CARBOHYD 189 189 INTERCHAIN (BY SIMILARITY).  
 FT CONFLICT 38 189 POTENTIAL.  
 FT CONFLICT 254 258 S -> T (IN REF. 1).  
 FT CONFLICT 276 276 VPSR -> APGG (IN REF. 1).  
 FT CONFLICT 321 321 A -> S (IN REF. 1).  
 FT CONFLICT 321 321 T -> A (IN REF. 1).  
 FT CONFLICT 384 384 S -> L (IN REF. 1).  
 SQ SEQUENCE 501 AA; 55640 MW; 712C0300 CRC32;

Query Match 98.5%; Score 3608; DB 1; Length 501;

Best Local Similarity 98.4%; Pred. No. 0.00e+00;

Matches 493; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 1 MRLPKLTLFWLWLDLEFICVLGAPDQGRPGQSGRGLAKAEKAPPLARNVFRP 60  
 QY 1 MRLPKLTLFWLWLDLEFICVLGAPDQGRPGQSGRGLAKAEKAPPLARNVFRP 60  
 Db 61 GHSYGGGATNANARAKGTTGQGLTQPKKDEPKLPPRPGGPEKPGHPQTRQATAR 120  
 QY 61 GHSYGGGATNANARAKGTTGQGLTQPKKDEPKLPPRPGGPEKPGHPQTRQATAR 120  
 Db 121 TVTPKGQLPGKAPKAGSVPSLLKAKREPGRPPPEKPPRPPPTTPHEYMLSLYRTL 180  
 QY 121 TVTPKGQLPGKAPKAGSVPSLLKAKREPGRPPPEKPPRPPPTTPHEYMLSLYRTL 180  
 Db 181 SDADRKGNSSVKLEAGLANTITSFIDKQDDRGVVRKQRYVEDISALEKDLGLGAEELR 240  
 QY 181 SDADRKGNSSVKLEAGLANTITSFIDKQDDRGVVRKQRYVEDISALEKDLGLGAEELR 240  
 Db 241 ILRKKPSDTAKPAPVPSRRRAAQLKSSCPGQRAALDVRSPGLDGSWEVFDIWKLF 300  
 QY 241 ILRKKPSDTAKPAPVPSRRRAAQLKSSCPGQRAALDVRSPGLDGSWEVFDIWKLF 300  
 Db 301 RNFKNQAQLCELEAWERGRVLDLGLGFDRAARQVHEKALFLVGRTRKRDLEFFNEIKA 360  
 QY 301 RNFKNQAQLCELEAWERGRVLDLGLGFDRAARQVHEKALFLVGRTRKRDLEFFNEIKA 360  
 Db 361 RSGQDDKTVYELFSQRRKRAPSATQGRKPSKNLAKRCSKALHVNFKDMGWDWIIIA 420  
 QY 361 RSGQDDKTVYELFSQRRKRAPSATQGRKPSKNLAKRCSKALHVNFKDMGWDWIIIA 420  
 Db 421 PLEYEAFHCEGLCEFFLRSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFID 480  
 QY 421 PLEYEAFHCEGLCEFFLRSHLEPTNHAVIOTLMNSMDPESTPTCCVPTRLSPISILFID 480  
 Db 481 SANNVYKQYEDMVESGCR 501  
 QY 481 SANNVYKQYEDMVESGCR 501

RESULT 2

ID GDF5\_MOUSE STANDARD; PRT; 495 AA.

AC P43027;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE GROWTH/DIFFERENTIATION FACTOR 5 PRECURSOR (GDF-5).  
 GN GDF5 OR GDF-5 OR BP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CD-1; TISSUE=EMBRYO;  
 RX MEDLINE; 94195427.  
 RA STORM E.F., HUYNH T.V., COPELAND N.G., JENKINS N.A., KINGSLEY D.M.,  
 RA LEE S.-J.;  
 RT "Limb alterations in brachypodism mice due to mutations in a new  
 member of the TGF-beta superfamily.";  
 RL Nature 368:639-643(1994).  
 CC -1- FUNCTION: COULD BE INVOLVED IN BONE FORMATION.  
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).  
 CC -1- DISEASE: DEFECTS IN GDF-5 ARE THE CAUSE OF BRACHYPODISM WHICH  
 ALTERS THE LENGTH AND NUMBERS OF BONES IN THE LIMBS BUT SPARES THE  
 AXIAL SKELETON.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 DR EMBL; U08337; AAA18778.1; -;  
 DR HSSP; P18075; IBMP.  
 DR MGD; MGI:95688; GDF5.  
 DR PROSITE; PS00250; TGF\_BETA; 1.  
 DR PFAM; PF00019; TGF-beta; 1.  
 DR PFAM; PF00688; TGF-beta; 1.  
 KW Signal; Growth factor; Cytokine; Glycoprotein; Polymorphism.  
 FT SIGNAL 1 ? POTENTIAL.  
 FT PROPEP ? 375 POTENTIAL.  
 FT CHAIN 376 495 GROWTH/DIFFERENTIATION FACTOR 5.  
 FT DISULFID 394 460 BY SIMILARITY.  
 FT DISULFID 423 492 BY SIMILARITY.  
 FT DISULFID 427 494 BY SIMILARITY.  
 FT DISULFID 459 459 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 183 183 POTENTIAL.  
 FT VARIANT 98 98 S -> P.  
 SQ SEQUENCE 495 AA; 54885 MW; F844574F CRC32;

Query Match 91.0%; Score 3332; DB 1; Length 495;  
 Best Local Similarity 91.2%; Pred. No. 0.00e+00;  
 Matches 457; Conservative 23; Mismatches 15; Indels 6; Gaps 2;

Db 1 MRLPKLTLFWLWLDLEFICVLGAPDQGRPGQSGRGLAKAEKAPPLARNVFRP 60  
 QY 1 MRLPKLTLFWLWLDLEFICVLGAPDQGRPGQSGRGLAKAEKAPPLARNVFRP 60  
 Db 61 GHSYGGGATNANARAKGTTGQGLTQPKKDEPKLPPRPGGPEKPGHPQTRQATAR 120  
 QY 61 GHSYGGGATNANARAKGTTGQGLTQPKKDEPKLPPRPGGPEKPGHPQTRQATAR 120  
 Db 115 TVTPKGQLPGKAPKAGSVPSLLKAKREPGRPPPEKPPRPPPTTPHEYMLSLYRTL 174  
 QY 115 TVTPKGQLPGKAPKAGSVPSLLKAKREPGRPPPEKPPRPPPTTPHEYMLSLYRTL 174  
 Db 121 TVTPKGQLPGKAPKAGSVPSLLKAKREPGRPPPEKPPRPPPTTPHEYMLSLYRTL 180  
 QY 121 TVTPKGQLPGKAPKAGSVPSLLKAKREPGRPPPEKPPRPPPTTPHEYMLSLYRTL 180  
 Db 175 SDADRKGNSSVKLEAGLANTITSFIDKQDDRGVVRKQRYVEDISALEKDLGLGAEELR 234  
 QY 175 SDADRKGNSSVKLEAGLANTITSFIDKQDDRGVVRKQRYVEDISALEKDLGLGAEELR 234  
 Db 181 SDADRKGNSSVKLEAGLANTITSFIDKQDDRGVVRKQRYVEDISALEKDLGLGAEELR 240  
 QY 181 SDADRKGNSSVKLEAGLANTITSFIDKQDDRGVVRKQRYVEDISALEKDLGLGAEELR 240  
 Db 235 ILRKKPSDTAKPAPVPSRRRAAQLKSSCPGQRAALDVRSPGLDGSWEVFDIWKLF 294  
 QY 235 ILRKKPSDTAKPAPVPSRRRAAQLKSSCPGQRAALDVRSPGLDGSWEVFDIWKLF 294  
 Db 241 ILRKKPSDTAKPAPVPSRRRAAQLKSSCPGQRAALDVRSPGLDGSWEVFDIWKLF 300  
 QY 241 ILRKKPSDTAKPAPVPSRRRAAQLKSSCPGQRAALDVRSPGLDGSWEVFDIWKLF 300





Query Match 22.7%; Score 832; DB 1; Length 125;  
Best Local Similarity 79.2%; Pred. No. 3.69e-152;  
Matches 99; Conservative 22; Mismatches 4; Indels 0; Gaps 0;

Db 1 RRRRTAFASRGHGRKSKRLSRKPLHVNFKELGWDWIIAPLEYAYHCEGVCDFF 60  
QY 377 RRRRAPLATRQGRKSRKALHVNFKDMGWDWIIAPLEYAYHCEGLCEFF 436  
Db 61 LRSHPLEPTNHAIQTLNMSMDPGSTPPSCCVPTKLTPTISILYIDAGNNVYKQYEDMVVE 120  
QY 437 LRSHPLEPTNHAVIQTLNMSMDPESTPPCCVPTRLSPISILFIDSANNVYKQYEDMVVE 496  
Db 121 SCGCR 125  
QY 497 SCGCR 501

RESULT 5  
ID GDF7\_MOUSE STANDARD; PRT; 151 AA.  
AC P43029;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE GROWTH/DIFFERENTIATION FACTOR 7 PRECURSOR (GDF-7) (FRAGMENT).  
GN GDF7 OR GDF-7.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C; TISSUE=LIVER;  
RX MEDLINE: 94195427.  
RA STORM E.E., HUYNH T.V., COPELAND N.G., JENKINS N.A., KINGSLEY D.M.,  
RA LEE S.-J.;  
RT "Limb alterations in brachypodism mice due to mutations in a new  
RT member of the TGF-beta-superfamily.";  
RL Nature 368:639-643(1994).  
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC EMBL: U08339; AAA18780.1; -.  
DR HSP: P18075; 1BMP.  
DR MGD: MGI-95690; GDF7.  
DR PROSITE; PS00250; TGF\_BETA; 1.  
DR PFAM; PF00019; TGF-beta; 1.  
KW Growth factor; Cytokine; Glycoprotein.  
FT NON\_TER <1 1  
FT PROPEP <1 5  
FT CHAIN 6 151  
FT DISULFID 50 116  
FT DISULFID 79 148  
FT DISULFID 83 150  
FT DISULFID 115 115  
FT DOMAIN 1 5  
FT DOMAIN 16 41  
SQ SEQUENCE 151 AA; 15697 MW; 62377F04 CRC32;  
FT POTENTIAL.  
FT GROWTH/DIFFERENTIATION FACTOR 7.  
FT BY SIMILARITY.  
FT BY SIMILARITY.  
FT BY SIMILARITY.  
FT INTERCHAIN (BY SIMILARITY).  
FT POLY-ARG.  
FT POLY-GLY.

Query Match 20.1%; Score 735; DB 1; Length 151;  
Best Local Similarity 74.3%; Pred. No. 3.01e-130;  
Matches 84; Conservative 24; Mismatches 5; Indels 0; Gaps 0;

Db 39 GRGHRGRRCRSKSLHVDKELGWDWIIAPLEYAYHCEGVCDFFPLRSLHLEPTNHAI 98  
QY 389 GRKPSKRLKARSKALHVNFKDMGWDWIIAPLEYAYHCEGLCEFFPLRSLHLEPTNHAV 448

Db 99 IQTLNMSMAPDAPASCVCVPARLSPISILYIDAGNNVYKQYEDMVVEAGCCR 151  
QY 449 IQTLNMSMDPESTPPCCVPTRLSPISILFIDSANNVYKQYEDMVVEAGCCR 501

RESULT 6  
ID BMP4\_CHICK STANDARD; PRT; 405 AA.  
AC Q90752;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4).  
GN BMP4 OR BMP-4.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;  
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WHITE LEGHORN;  
RX MEDLINE: 94163974.  
RA FRANCIS P.H., RICHARDSON M.K., BRICKELL P.M., TICKLE C.;  
RT "Bone morphogenetic proteins and a signalling pathway that controls  
RT patterning in the developing chick limb.";  
RL Development 120:209-218(1994).

CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.  
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC EMBL: X75915; CAA53514.1; -.  
DR HSP: P18075; 1BMP.  
DR PROSITE; PS00250; TGF\_BETA; 1.  
DR PFAM; PF00019; TGF-beta; 1.  
DR PFAM; PF00688; TGF-beta; 1.  
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.  
FT SIGNAL 1 19  
FT PROPEP 20 291  
FT CHAIN 292 405  
FT DISULFID 305 370  
FT DISULFID 334 402  
FT DISULFID 338 404  
FT DISULFID 369 369  
FT CARBOHYD 144 144  
FT CARBOHYD 208 208  
FT CARBOHYD 347 347  
FT CARBOHYD 362 362  
SQ SEQUENCE 405 AA; 46057 MW; A60C5A50 CRC32;

Query Match 15.5%; Score 566; DB 1; Length 405;  
Best Local Similarity 32.2%; Pred. No. 1.32e-92;  
Matches 130; Conservative 89; Mismatches 152; Indels 33; Gaps 27;

Db 23 HASLIPETGRKKVAELQAGSGRRSAQSHELLRGFTTLLQFGLRRRP-QPSKSA-VI 80  
QY 110 HPPQTRQATARTVP-KGOLPGGRAPPKAGSVPSFLKKAREPGPPREPKEPFPPT 168  
Db 81 P-STYMLDYLRLQSGEEERSLQEIISLOYPERSASRANTVRSFHEEHLESVPGSEAPRI 139  
QY 169 PHEMYLSLYRTLS--DADRKGNGNSVKL-E--AGLANTITSFDKGO-DD-RGPV-VRKQ 220  
Db 140 RFVNLSSVPDNEVISSEELRLYREQVEEPSAAMERGFHRINIYVMKPLSERSQAIFRL 199  
QY 221 RYVEDISAL-EXDGLLGAELRLKPKSDTAKPAAPGGGAAQKLKSCPSGR-OPAS-L 277  
Db 200 LDTRLVH-HNVTRWETFDVSPAVIRWTKDKQPNHGLVI-E---VTHLHQAQ-THQGRHVR 253

QY 278 LDVRSVPLGSDGWEVFIWIKLFRNFKNSAQLCLELEAWERGRAVDLRGLGFDRAARQVH 337  
 Db 254 I-SRSLPQGHGQWAL-RPLLVTTCHDGRG-HA-L-T-RRARRSP--KHHGSR--KN-K 302  
 QY 338 EKALVELVGRTKKRLFFNEIKARSGQDDKTYEYLFSSQRRRRAPLATROGKRPSKNLJK 397  
 Db 303 KNCRRHALYVDFSDVGNWDIIVAPCYQAFYCHGCPPLADHLNSTHAIIVOTLVNSVN 362  
 QY 398 ARCSRKALHVNFKDGDWDIIAPLEYAFHCEGLCEFLRSHLEPTNHAVIQTLMNSMD 457  
 Db 363 S-SIPKACCVPTSELSAISMLYDEYDKVVKYQKVMVGGCCRC 405  
 QY 458 PESTPTCCVPTRLSPISILFIDSANNVYKQYEDVMVGGCCRC 501

RESULT 7  
 ID BMP2\_DAWDA STANDARD; PRT: 396 AA.  
 AC 019006;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2).  
 GN BMP2.  
 OS Dama dama (Fallow deer) (Cervus dama).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae; Cervinae;  
 OC Cervinae; Cervus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=ANTLER;  
 RX MEDLINE; 97157076.  
 RA FENG J.Q., CHEN D., GHOSH-CHOUDHURY N., ESPARZA J., MUNDY G.R.,  
 RA HARRIS S.E.;  
 FT "Bone morphogenetic protein 2 transcripts in rapidly developing deer  
 FT antler tissue contain an extended 5' non-coding region arising from a  
 FT distal promoter.";  
 FT Biochim. Biophys. Acta 1350:47-52(1997).  
 CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.  
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.  
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC [1]  
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 CC -----  
 CC EMBL: AJ001817; CAA05033.1; -  
 CC HSP: P18075; 1BMP.  
 CC PROSITE: PS00250; TGF\_BETA; 1.  
 CC PFAM: PF00688; TGF-beta; 1.  
 CC Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.  
 CC SIGNAL 1 ?  
 CC PROPEP ?  
 CC CHAIN 283  
 CC DISULFID 296 361  
 CC DISULFID 325 393  
 CC DISULFID 329 395  
 CC DISULFID 360 360  
 CC DISULFID 135 135  
 CC CARBOHYD 163 163  
 CC CARBOHYD 164 164  
 CC CARBOHYD 200 200  
 CC CARBOHYD 338 338  
 CC SEQUENCE 396 AA; 44646 MW; 8C56358B CRC32;

DR HSP: P18075; 1BMP.  
 DR PROSITE: PS00250; TGF\_BETA; 1.  
 DR PFAM: PF00688; TGF-beta; 1.  
 DR Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.  
 DR SIGNAL 1 ?  
 DR PROPEP ?  
 DR CHAIN 283  
 DR DISULFID 296 361  
 DR DISULFID 325 393  
 DR DISULFID 329 395  
 DR DISULFID 360 360  
 DR DISULFID 135 135  
 DR CARBOHYD 163 163  
 DR CARBOHYD 164 164  
 DR CARBOHYD 200 200  
 DR CARBOHYD 338 338  
 DR SEQUENCE 396 AA; 44646 MW; 8C56358B CRC32;  
 Query Match 15.4%; Score 565; DB 1; Length 396;  
 Best Local Similarity 32.3%; Pred. No. 2.20e-92;  
 Matches 124; Conservative 97; Mismatches 127; Indels 36; Gaps 31;

Db 38 PGRSSSQSDVLSSEFLRLSMFGLKQRPPT-PSRDP-VVPP-YMLDLYR-LHSGOPGAP 93  
 QY 129 PGKAPPRKAGSPVSSFLAKAREPGPPRPKEPFRPPITPHEYMUSLYRTLSADARKGG 188  
 Db 94 APCHRLRAASLANVTRTFHHEESLEELPEMGKTTTRFFFLNLTSTPTFEFTTSAELOVF 153  
 QY 189 NSSVKLE--AGLANITTSFI-DKGQDDRGV-V-RK-QRYVFDISALEKDGGLL-GAELRIL 242  
 Db 154 GKHPPEALENNSSPHIRINIFEIIRPATANSKPPVTRLLDTRLVTO-NASRWESFDV-TP 211  
 QY 243 RKKSDTAKPAAPGGGAAQLKL--SSCPSGROPAS-LLDVRSPVGLDGSWEVFIWIKL 299  
 Db 212 -AVMRWTAQG-LTNHGFV-V-EVAHPEDSYGAKRHVRISRLHSDHSHWSQIRPLL--- 264  
 QY 300 FRNFKNSAQLCLELEAWERGRAVDLRGLGFDRAARQVH-EKALFL-VFGRTKKRLDFFNE 357  
 Db 265 V-T-FGHDKGK-HP-L--HREKR-Q-A-KH-QKR-KRLKSSCKRHPLYVDFSDVGNWDW 313  
 QY 358 IKARSGQDDKTYEYLFSSQRRRRAPLATROGKRPSKNLKAARSKALHVNFKDGDWDW 417  
 Db 314 IVAPFGYHAFYCHGCPPLADHLNSTHAIIVOTLVNSVNSK-IPKACCVPTSELSAISML 372  
 QY 418 IIAPLEYAFHCEGLCEFLRSHLEPTNHAVIQTLMNSMDPESTPTCCVPTRLSPISIL 477  
 Db 373 YLDENEKVVVKYQKVMVGGCCRC 396  
 QY 478 FIDSANNVYKQYEDVMVGGCCRC 501  
 RESULT 8  
 ID BMP2\_RAT STANDARD; PRT: 393 AA.  
 AC P49001;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (BMP-2A).  
 GN BMP2 OR BMP-2  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BONE;  
 RA FENG J.Q., CHEN D., FENG M., HARRIS M.A., MUNDY G.R., HARRIS S.E.;  
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.  
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.  
 CC -!- TISSUE SPECIFICITY: FEMUR, CALVARIA, TRACHEA, LUNG AND OVARY.  
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
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 CC -----  
 CC EMBL: Z25868; CAA81088.1; -  
 CC HSP: P18075; 1BMP.  
 CC PROSITE: PS00250; TGF\_BETA; 1.  
 CC PFAM: PF00019; TGF-beta; 1.  
 CC PFAM: PF00688; TGF-beta; 1.  
 CC Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.  
 CC SIGNAL 1 ?  
 CC PROPEP ?  
 CC CHAIN 280 393  
 CC DISULFID 293 358  
 CC DISULFID 322 390  
 CC DISULFID 326 392  
 CC DISULFID 357 357  
 CC CARBOHYD 133 133  
 CC CARBOHYD 161 161  
 CC SEQUENCE 393 AA; 44646 MW; 8C56358B CRC32;

FT	DISULFID	328	394	BY SIMILARITY.
FT	DISULFID	359	359	INTERCHAIN (BY SIMILARITY).
FT	CARBOHYD	134	134	POTENTIAL.
FT	CARBOHYD	199	199	POTENTIAL.
FT	CARBOHYD	337	337	POTENTIAL.
SEQ	SEQUENCE	395 AA;	44664 MW; 81F38FIE CRC32;	
Query Match 14.9%; Score 544; DB 1; Length 395;				
Best Local Similarity 31.1%; Pred.No.9.04e-88;				
Matches 119; Conservative 98; Mismatches 133; Indels 33; Gaps				
Db	36	SSGRSPQSDDDILSFEURLLSMFLGKORPT-PSRDA-VVPP-YMLDLYRRHSGQFGAP	92	
QY	129	PGKAPPKAGS-VPSFLLKKAREPGPREPKPPRPPTTPHEYMLSYRTLS-DADRK	186	
Db	93	APDHLRLAASRANTVRSFHHSESLEELPETSQTKTTRFFFNLTSPPEFITSAELOVF	152	
QY	187	GGNSSVKYLEAGLANTTSFT-DKGDD-RGPVVRK-ORVFDISALEKDGLL-GAEIRL	242	
Db	153	REQMQEALGDDSGFHHIRINYEIKPATANSKPPATRLLDTRLV-NQNTSRWESFDVTPA	211	
QY	243	RKPSDTAKPAAPGGGAA--QLKLSGSGGROPAS-LIDVRSVPGDLSGHEVFDIWL	299	
Db	212	VMRTAQGHANHFVV-EVTHLEEKGVG-KRHVR-I-SRSLHPDSEHSQIRPLL--V	264	
QY	300	FRNFKNSAQLCLEAWERGRAVDLRLGLGFDRAARQVHEKALF-VFGRTKKRDLFFNEI	358	
Db	265	-T-FGDHKG-HP-L-HRREKR-Q-A-KH-QOR-KELKSSCKRRHPLYVDFSDVGHNDWI	313	
QY	359	KARSGQDKTVYELFYSQRKKRAPLATQGRKPSNLKARC SRKALHNFKMDGWDWI	418	
Db	314	VAPPGYHAFYCHCECPFLADHLNSTHNAVOTLVNSVNSK-IPKACCVPTLSAISMLY	372	
QY	419	IAPLEYAFHCEGLCEPFLSHLEPNHNAVITQTLMSMDPESTPTCCVPTRLSPISILF	478	
Db	373	LDENEKVLKYNQDMVVEGCGCR	395	
QY	479	IDSANNVYKQYEDMVVSGCR	501	
RESULT 10				
ID	BMP2_HUMAN	STANDARD;	PRT;	396 AA.
AC	P12643;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	15-DEC-1999 (Rel. 39, Last annotation update)			
DE	BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (BMP-2A).			
GN	BMP2 OR BMP2A.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 89072730.			
RA	WOZNED J.W., ROSEN V., CELESTE A.J., MITSOCK L.M., WHITTERS M.J.,			
RA	KRIZ R.J., HEWICK R.M., WANG E.A.;			
RT	"Novel regulators of bone formation: molecular clones and			
RT	activities.";			
RL	Science 242:1528-1534(1988).			
RN	[2]			
RP	X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 292-396.			
RX	MEDLINE; 99175323.			
RA	SCHUEFLER C., SEBALD W., HUELSMEYER M.;			
RT	"Crystal structure of human bone morphogenetic protein-2 at 2.7 A			
RT	resolution.";			
RL	J. Mol. Biol. 287:103-115(1999).			
CC	-!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.			
CC	-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.			
CC	-!- TISSUE SPECIFICITY: PARTICULARLY ABUNDANT IN LUNG, SPLEEN AND			
CC	COLON AND IN LOW BUT SIGNIFICANT LEVELS IN HEART, BRAIN, PLACENTA			
CC	LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS, PROSTATE, OVARY AND			
CC	SMALL INTESTINE.			
CC	-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.			

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-----  
EMBL; M22489; AAA51834.1; -;  
DR PIR; B37278; B37278.  
DR HSP; P18075; IBMP.  
DR MIN; 112261; -;  
DR PDB; 2BMP; 18-SEP-99.  
DR PROSITE; PS00250; TGF\_BETA; 1.  
DR PFAM; PF00019; TGF-beta; 1.  
DR PFAM; PF00688; TGF-beta; 1.  
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein;  
KW 3D-structure.  
FT SIGNAL 1 ? POTENTIAL.  
FT PROPEP 282  
FT CHAIN 283 396 BONE MORPHOGENETIC PROTEIN 2.  
FT DISULFID 296 361  
FT DISULFID 325 393  
FT DISULFID 329 395  
FT DISULFID 360 360 INTERCHAIN.  
FT CARBOHYD 135 135 POTENTIAL.  
FT CARBOHYD 163 163 POTENTIAL.  
FT CARBOHYD 164 164 POTENTIAL.  
FT CARBOHYD 200 200 POTENTIAL.  
SQ SEQUENCE 396 AA; 44702 MW; 182782C0 CRC32;  
  
Query Match 14.9%; Score 546; DB 1; Length 396;  
Best Local Similarity 31.1%; Pred. No. 3.29e-88;  
Matches 119; Conservative 100; Mismatches 131; Indels 33; Gaps 29;  
  
Db 37 SSGRSPSPSDVLSFELRLLSMFLKORPT-PSRDA-VVPP-YMLDLRYRHSGQSP 93  
QY 129 PGKAPPRAGS-VPSFLKKAREPGPREPEPPPTIPHEYMLSLYRTLS-DADRK 186  
Db 94 APDKLERAASRANTVRSFHHSEELPETSGKTRRFFNNLSSIPTEFTTSALQV 153  
QY 187 GGNSSVKLEAGLANITFSI-DKGQDD-RGPVVRK-QRYVFDISALEKDGLL-GAELRL 242  
Db 154 RQMDALGNNSFHRNIYIIPATANSKEPTRLDRLV-NQNASRWESEDTVPA 212  
QY 243 RKKPSDTAKPAAPGGGAA--QKLSSCSPSGROPAS-LLDVRSPGLDGSWEVDFWKL 299  
Db 213 VMRTAQGHANHFVY-EVAHLEEQVY-KRHR-I-SRSLHQDEHSWSQIRPLL--V 265  
QY 300 FRNFKNQAQLCLEAWERGRAVDLGLGFDRAARQVHEKALFL-VFGTKKRDLFFNEI 358  
Db 266 -T-FGHDKGK-HP-L--HKREKR-Q-A-KH-KOR-KRLKSSCKRHPLYVDFSDVGNNDWI 314  
QY 359 KARSQDDKTVYELFSQRRKRRAPIATQGRKPSKRLKARCSKALHVNFKDMGDDWI 418  
Db 315 VAPPGYHAFYCHGECFPPLADHLNSTNHAIVOTLVNSVNSK-IPKACCVPTLSAISMLY 373  
QY 419 IAPLEYAFHCEGLCEFFPLRSHLEPTNHAIVQITLMSMDPESTPTCCVPTRLSPILF 478  
Db 374 LDENEKVLKNYQDMVVEGCGCR 396  
QY 479 IDSANNVYQYEDMVVEGCGCR 501  
  
RESULT 11  
ID BMA\_XENLA STANDARD; PRT; 398 AA.  
AC P25703;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 01-JUL-1993 (Rel. 26, Last annotation update)  
DE BONE MORPHOGENETIC PROTEIN 2-I PRECURSOR (BMP-2-I).  
OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;  
OC Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae;  
OC Xenopus.  
RN [1]  
RX SEQUENCE FROM N.A.  
RP MEDLINE; 91274367.  
RT "cDNA sequence of Xenopus laevis bone morphogenetic protein 2 (BMP-2)."  
RL Biochim. Biophys. Acta 1089:280-282(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 92378616.  
RA NISHIMATSU S., SUZUKI A., SHODA A., MURAKAMI K., UENO N.;  
RT "Genes for bone morphogenetic proteins are differentially transcribed in early amphibian embryos."  
RL Biochem. Biophys. Res. Commun. 186:1487-1495(1992).  
CC !- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.  
CC !- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.  
CC !- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
CC -----  
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CC -----  
DR EMBL; X55031; CAA38850.1; -;  
DR EMBL; X63424; CAA45018.1; -;  
DR PIR; S16244; S16244.  
DR PIR; JH0687; JH0687.  
DR HSP; P18075; IBMP.  
DR PROSITE; PS00250; TGF\_BETA; 1.  
DR PFAM; PF00019; TGF-beta; 1.  
DR PFAM; PF00688; TGF-beta; 1.  
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.  
FT SIGNAL 1 ? POTENTIAL.  
FT PROPEP 284  
FT CHAIN 285 398 BONE MORPHOGENETIC PROTEIN 2-I.  
FT DISULFID 298 363 BY SIMILARITY.  
FT DISULFID 327 395 BY SIMILARITY.  
FT DISULFID 331 397 BY SIMILARITY.  
FT DISULFID 362 362 INTERCHAIN (BY SIMILARITY).  
FT CARBOHYD 137 137 POTENTIAL.  
FT CARBOHYD 202 202 POTENTIAL.  
FT CARBOHYD 340 340 POTENTIAL.  
FT CONFLICT 7 7 S -> P (IN REF. 2).  
FT CONFLICT 16 16 V -> L (IN REF. 2).  
FT CONFLICT 233 233 N -> T (IN REF. 2).  
SQ SEQUENCE 398 AA; 45575 MW; 6143F996 CRC32;  
  
Query Match 14.9%; Score 545; DB 1; Length 398;  
Best Local Similarity 32.7%; Pred. No. 5.46e-88;  
Matches 126; Conservative 88; Mismatches 136; Indels 35; Gaps 28;  
  
Db 36 SGRSSPQSQSORVLNOFELRLLSMFLKRRPT-PGKNVVIIP--YMLDLYHLHLAQLAADE 92  
QY 130 GCKAPPKAG-SVPSFLLKKAREPGPREPEPPPTIPHEYMLSLYRT-LSDADRGK 187  
Db 93 GTSAMDQWERAASRANTVRSFHHSEMEIEPESREKTIQRFNNLSSIPNEELVTSABL 152  
QY 188 GNSV--KLE--AGLANITTSFI-DKGQDD-RGPVVRK-QRYVFDISALEKDGLL-GAEL 239  
Db 153 RIFREQVQEPFESSKLRINIYDIVKPAASRGVVRVLLDRLVH-HNESKWSFV 211  
QY 240 RIIRKKPSDTAKPAAPGGGAAQLKL--SCFSGROPA-SLLDVRSPGLDGSWEVFDI 296  
Db 212 -TPAIA-RWIAH---K-QP-NHGFVVEVNHLDNKNVKKHVR-ISRSLTPDKNMPQIR 263  
QY 297 WKLFERNKNSAQLCLEAWERGRAVDLGLGFDRAARQVHEKALFLVFGTKKRDLFFN 356

Db 264 PLLVTFSDGKG-HA-L--HKROKR-Q-A-RH-KOR-KRLKSSRRHPLVYDFSDGVND 314  
 QY 357 EIKARSQDDTYVEYFSQRRKRRLATPQGRPSKRLKARSRKALHVNFKDMGWDD 416  
 Db 315 WIVAPPYHAFYCHGCEFPPLADHLNSTHNAIVQTLVNSVNTN-IPKACCVPTLSAISM 373  
 QY 417 WIIAPLEYAFHCEGLCEFPPLSHLEPTNHAIVQTLNMSNDPESTPTCCVPTRLSPISI 476  
 Db 374 LYLDENEKVLNLYQDMVVECCGR 398  
 QY 477 LFIDSANNVYKQYEDMVVESCGR 501

RESULT 12  
 ID BMP5\_MOUSE STANDARD; PRT; 452 AA.  
 AC P49003;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 L BONE MORPHOGENETIC PROTEIN 5 PRECURSOR (BMP-5).  
 GN BMP5 OR BMP-5.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RC STRAIN-C3H/KW;  
 RX MEDLINE; 95046894.  
 RA KING J.A., MARKER P.C., SEUNG K.J., KINGSLEY D.M.;  
 RT "BMP5 and the molecular, skeletal, and soft-tissue alterations in  
 short ear mice."  
 RL Dev. Biol. 166:112-122(1994).  
 CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.  
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC [1]  
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 CC -----  
 DR EMBL; L41145; AAA64612.1; .  
 DR HSP; P18075; IBMP.  
 DR MGD; MGI:88181; BMP5.  
 DR PROSITE; PS00250; TGF-BETA; 1.  
 DR PFAM; PF00019; TGF-beta; 1.  
 DR PFAM; PF00688; TGF-beta; 1.  
 KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.  
 FT SIGNAL 1 ?  
 FT PROPEP ? 320  
 FT CHAIN 321 452  
 FT DISULFID 351 417  
 FT DISULFID 380 449  
 FT DISULFID 384 451  
 FT DISULFID 416 416  
 FT CARBOHYD 209 209  
 FT CARBOHYD 325 325  
 FT CARBOHYD 343 343  
 FT CARBOHYD 393 393  
 SQ SEQUENCE 452 AA; 51511 MW; 62BFED17 CRC32;

Query Match 14.9%; Score 546; DB 1; Length 452;  
 Best Local Similarity 28.8%; Pred. No. 3.29e-88;  
 Matches 107; Conservative 101; Mismatches 140; Indels 24; Gaps 23;  
 Db 94 PEEVLVR-VSLAGEAKETKRGYPASP-NGYAHRLHLPPRTPLTTQSPPLASLHDTNFND 151  
 QY 141 PSSFLKKAREPGGPEKPEKPPPTTPHEYMLSLY-RT-LS-DADRKGNGSSVKLEAG 197  
 Db 152 -ADMVMSFVNLVERKDPFSHQRRHYKEPRFDLTQIPHCEAVTAAEFRIYKDKGNHRFENE 210

QY 198 LANTITFIDKGQDDRG-PVVRKQ-R-YVEDISALER-DGLLGAELRLLRKKPSDTAKPA 253  
 Db 211 TIKIS-TYQI-IKEY-TNRDADFLDTRKTQALD-VGWLVDITVTSNHWVINPQNLG 266  
 QY 254 APGGRAQLKLSGPCSGROPA-SLLDVRSPVGLDGSWEVFDIWKLFNRP-KNS-AQLC 310  
 Db 267 LOLCAETGDCRSINVKSAGLV-GRHGQSQKOPFMV-AFFKASEVLLRSVRAASRKNONR 324  
 QY 311 LEL-EAWERGRAVDLGLGDFDRAARQVHEKALFLVFGTKRDLFFNEIKARSQDDKTV 369  
 Db 325 NKSX-SHQDPSRM-P-SA--GDYNTSEQACKKHELXVSFRDLGWQDWIAPGYAAYFC 380  
 QY 370 YEYLFQRRKRRLATPQGRPSKRLKARSRKALHVNFKDMGWDDWIIAPLEYAFHC 429  
 Db 381 DGECSFPLNHNATNHAIVQTLVHLMFPDPHVPRKPCAPTKLNAISLYPDDSSNVILKK 440  
 QY 430 EGLCEFFLRSHLEPTNHAIVQTLNMSNDPESTPTCCVPTRLSPISILFIDSANNVYKQ 489  
 Db 441 YRNMVRSQCGCH 452  
 QY 490 YEDMVVESCGR 501

RESULT 13  
 ID BMP5\_HUMAN STANDARD; PRT; 454 AA.  
 AC P22003;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE BONE MORPHOGENETIC PROTEIN 5 PRECURSOR (BMP-5).  
 GN BMP5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC TISSUE-BONE;  
 RX MEDLINE; 91088608.  
 RA CELESTE A.J., IANNAZZI J.A., TAYLOR R.C., HEWICK R.M., ROSEN V.,  
 RA WANG E.A., WOZNEY J.M.;  
 RT "Identification of transforming growth factor beta family members  
 present in bone-inductive protein purified from bovine bone."  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).  
 CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.  
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE LUNGS AND LIVER.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; M60314; AAA36736.1; .  
 DR PIR; A39263; A39263.  
 DR HSP; P18075; IBMP.  
 DR MIM; I12265; .  
 DR PROSITE; PS00250; TGF-BETA; 1.  
 DR PFAM; PF00019; TGF-beta; 1.  
 DR PFAM; PF00688; TGF-beta; 1.  
 KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.  
 FT SIGNAL 1 ?  
 FT PROPEP ? 322  
 FT CHAIN 323 454  
 FT DISULFID 353 419  
 FT DISULFID 382 451  
 FT DISULFID 386 453  
 FT DISULFID 418 418  
 FT CARBOHYD 211 211

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FT CARBOHYD 327 327 POTENTIAL.
FT CARBOHYD 345 345 POTENTIAL.
FT CARBOHYD 395 395 POTENTIAL.
SQ SEQUENCE 454 AA; 51736 MW; 559AC82B CRC32;

Query Match 14.8%; Score 543; DB 1; Length 454;
Best Local Similarity 30.8%; Pred. No. 1.50e-87;
Matches 96; Conservative 88; Mismatches 108; Indels 20; Gaps 18;

Db 154 ADMVMSFNLVERDKSHQRHYKFERDLTQIPHEAVTAARFYKORSNNRNET 213
QY 199 ANTITSIDRGQDRG-PVVRKQ-R-YVFDISALEK-DGLGAEILRLKPKSPAKPAA 254
Db 214 IKIS-IYQI-IKEY-TNRDADFLLTRKAQALD-VGWLVDITVTSNHWVINPNLGL 269
QY 255 PGGRAQLKSLSCPSGRQPA-SLLDVSVPGLDGSWEVFDIWKLFNF-KNS-AQLCL 311
Db 270 QLCATGDSRINYSKAGL--VGRQSQSQKPPMV-AFFKASEVLLRSVRAANKRKNR 326
QY 312 EL-EAWERGRAVDLRLGLGDFDRAARQV-HEKALFLVFGTRKRLDFFNEIKARSGDDKTV 369
Db 327 NKS-SSHODSR--MSSV-GDYNTSEKQACKKELVYSPDLGQWDWIAPGYAAYFC 382
QY 370 YEYLSQRRKRRLAPLQTRQGRKPSKNLKRCSKALHVNFKMDGWDWIAPLEYAFHC 429
Db 383 DGECSFPLNHNATNAIVOTLVHLPDPDHVPKPCCAPTKLNAISVLVYDDSSNVILKK 442
QY 430 EGLCEFLRLSHLEPTNHAIVQTLNMSMDPESTPTCCVPTRLSPISILFIDSANNVYKQ 489
Db 443 YRNVVRSCGCH 454
QY 490 YEDMVVESCGR 501

RESULT 14
ID BMP2_MOUSE STANDARD; PRT; 394 AA.
AC P2127A;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (BMP-2A).
GN BMP2 OR BMP-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RX SEQUENCE FROM N.A.
RP MEDLINE; 94289485.
RA FENG J.Q., HARRIS M.A., GHOSH-CHOUDHURY N., FENG M., MUNDY G.R.,
RA HARRIS S.E.;
RT "Structure and sequence of mouse bone morphogenetic protein-2 gene
RT (BMP-2): comparison of the structures and promoter regions of BMP-2
RT and BMP-4 genes."
RL Biochim. Biophys. Acta 1218:221-224(1994).
RN [2]
RP SEQUENCE OF 1-351 FROM N.A.
RX MEDLINE; 90228966.
RA DICKINSON M.E., KOBRIN M.S., SILAN C.M., KINGSLEY D.M., JUSTICE M.J.,
RA MILLER D.A., CECI J.D., LOCK L.F., LEE A., BUCHBERG A.M.,
RA STRACUSA L.D., LYONS K.M., DERYNCK R., HOGAN B.L.M., COPELAND N.G.,
RA JENKINS N.A.;
RT "Chromosomal localization of seven members of the murine TGF-beta
RT superfamily suggests close linkage to several morphogenetic mutant
RT loci."
RL Genomics 6:505-520(1990).
CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
CC EMBL; X63425; CAA45019.1; -
DR PIR; JH0688; JH0688.
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CC -----
CC EMBL; L25602; AAB05665.1; -
DR PIR; A34201; A34201.
DR HSP; P18075; IBMP.
DR MGD; MGI-88177; BMP2.
DR PROSITE; PS00250; TGF_BETA; 1.
DR PFAM; PF00019; TGF-beta; 1.
DR PFAM; PF00688; TGF_beta_propeptide; 1.
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 ?
FT PROPEP ? 280
FT CHAIN 281 394 BONE MORPHOGENETIC PROTEIN 2.
FT DISULFID 294 359 BY SIMILARITY.
FT DISULFID 323 391 BY SIMILARITY.
FT DISULFID 327 393 BY SIMILARITY.
FT DISULFID 358 358 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 134 134 POTENTIAL.
FT CARBOHYD 162 162 POTENTIAL.
FT CARBOHYD 198 198 POTENTIAL.
FT CARBOHYD 336 336 POTENTIAL.
FT CONFLICT 110 110 T -> S (IN REF. 2).
FT CONFLICT 113 114 QL -> HE (IN REF. 2).
FT CONFLICT 271 271 G -> R (IN REF. 2).
SQ SEQUENCE 394 AA; 44514 MW; B055A5A9 CRC32;

Query Match 14.6%; Score 533; DB 1; Length 394;
Best Local Similarity 55.2%; Pred. No. 2.33e-85;
Matches 64; Conservative 25; Mismatches 25; Indels 2; Gaps 2;

Db 280 RQAKHKORKRLKSKRHLVYDFSDVGNWIMVAPPGYHAFYCHGECFPFLADHLNSTN 339
QY 387 RQGR-RPSKRLKARCSKRALHVNFKMDGWDWIAPLEYAFHCGLCEFLRLSHLEPTN 445
Db 340 HAIYOTLVNSVNSK-IPKACCVPTELSAISMLYLDENEKVKLVKDYQDMVVEGCGCR 394
QY 446 HAVIOTLMSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501

RESULT 15
ID BMPX_XENLA STANDARD; PRT; 398 AA.
AC P30884;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2-II PRECURSOR (BMP-2-II).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92378616.
RA NISHIMATSU S., SUZUKI A., SHODA A., MURAKAMI K., UENO N.;
RT "Genes for bone morphogenetic proteins are differentially transcribed
RT in early amphibian embryos."
RL Biochem. Biophys. Res. Commun. 186:1487-1495(1992).
CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
CC EMBL; X63425; CAA45019.1; -
DR PIR; JH0688; JH0688.
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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Apr 19 19:49:04 2000; MasPar time 23.94 Seconds  
838.682 Million cell updates/sec  
Output not generated.

Title: >US-09-297-092-1  
Description: (1-501) from US09297092.ppep  
Perfect Score: 3662  
Sequence: 1 MRLPKLTLFWLWLDLE.....ANNVYKQYEDMVVSCGCR 501

Scoring table: PAM 150  
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir62  
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 49.502; Variance 103.098; scale 0.480

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3662	100.0	501	2	JC2347 growth/differentiatio	0.00e+00
2	3608	98.5	501	2	A55452 cartilage-derived mor	0.00e+00
3	3332	91.0	495	2	S43294 bone morphogenetic pr	0.00e+00
4	939	25.6	436	2	B55452 cartilage-derived mor	4.37e-153
5	832	22.7	125	2	S43295 bone morphogenetic pr	5.74e-132
6	735	20.1	151	2	S43296 bone morphogenetic pr	5.80e-113
7	566	15.5	405	2	I50608 bone morphogenetic pr	2.69e-80
8	544	14.9	393	2	S37073 bone morphogenetic pr	4.23e-76
9	546	14.9	396	1	BMH07 bone morphogenetic pr	4.23e-76
10	544	14.9	398	2	JH0687 bone morphogenetic pr	4.23e-76
11	546	14.9	452	2	I49542 bone morphogenetic pr	1.76e-76
12	543	14.8	454	1	BMH05 bone morphogenetic pr	6.56e-76
13	533	14.6	394	2	S45355 bone morphogenetic pr	5.24e-74
14	536	14.6	398	2	JH0688 bone morphogenetic pr	1.41e-74
15	533	14.6	408	1	BMH04 bone morphogenetic pr	5.24e-74
16	532	14.5	408	2	S58791 bone morphogenetic pr	8.11e-74
17	530	14.5	408	2	S38343 bone morphogenetic pr	1.95e-73
18	530	14.5	420	2	I49541 bone morphogenetic pr	1.95e-73
19	529	14.4	400	2	A49147 bone morphogenetic pr	3.01e-73
20	529	14.4	401	2	JH0689 bone morphogenetic pr	3.01e-73
21	525	14.3	588	2	A26158 decapentaplegic prote	1.73e-72
22	515	14.1	353	2	I50607 bone morphogenetic pr	1.36e-70
23	516	14.1	408	2	JH0801 bone morphogenetic pr	8.81e-71

24	517	14.1	461	2	S52408	SPDVRL protein - sea	5.69e-71
25	512	14.0	431	1	BMH07	bone morphogenetic pr	5.04e-70
26	509	13.9	313	2	I51284	bone morphogenetic pr	1.86e-69
27	509	13.9	430	2	JQ1184	osteogenic protein 1	1.86e-69
28	498	13.6	402	2	A45056	osteogenic protein 2	2.23e-67
29	491	13.4	207	2	S37618	vgr protein - rat (fr	4.67e-66
30	489	13.4	426	2	JH0690	bone morphogenetic pr	1.11e-65
31	491	13.4	513	1	BMH06	bone morphogenetic pr	4.67e-66
32	488	13.3	510	2	A54798	Vg-1-related protein	1.72e-65
33	471	12.9	427	2	A40735	TGF beta homolog dsl-	2.69e-62
34	469	12.8	360	2	A29619	Vg1 embryonic growth	6.39e-62
35	459	12.5	455	2	A43918	TGF-beta-related prot	4.77e-60
36	433	11.8	360	2	I53032	bone morphogenetic pr	3.36e-55
37	433	11.8	472	1	BMH03	bone morphogenetic pr	3.36e-55
38	419	11.4	476	2	JC4546	bone morphogenetic pr	1.33e-52
39	414	11.3	357	2	A39364	GDF-1 embryonic growt	1.12e-51
40	415	11.3	478	2	JC4838	bone morphogenetic pr	7.29e-52
41	409	11.2	366	2	A46607	growth/differentiatio	9.35e-51
42	411	11.2	372	2	C39364	GDF-1 embryonic growt	3.99e-51
43	402	11.0	366	2	A45402	transforming growth f	1.82e-49
44	364	9.9	354	2	S29718	gene nodal protein -	1.62e-42
45	351	9.6	79	2	S21473	transforming growth f	3.65e-40

ALIGNMENTS

RESULT	1	JC2347	#type complete
ENTRY		growth/differentiation factor 5 - human	
TITLE		#formal_name Homo sapiens #common_name man	
ORGANISM		20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change	
DATE		09-Apr-1998	
ACCESSIONS		JC2347	
REFERENCE		JC2347	
#authors		Hoetten, G.; Neidhardt, H.; Jacobowsky, B.; Pohl, J.	
#journal		Biochem. Biophys. Res. Commun. (1994) 204:646-652	
#title		Cloning and expression of recombinant human	
		growth/differentiation factor 5.	
#accession		JC2347	
#molecule_type		DNA	
#residues		1-501	#label HOE
GENETICS			
#gene		GDB:BMP9	
#cross-references		GDB:433948	
#introns		211/1	
KEYWORDS		glycoprotein	
FEATURE			
189			

381-382	#binding_site carbohydrate (Asn) (covalent) #status	
	predicted	
	#cleavage_site Arg-Ala (unidentified proteinase) #status	
	predicted	
SUMMARY	#length 501 #molecular-weight 55410 #checksum 5334	
	Query Match 100.0%; Score 3662; DB 2; Length 501;	
	Best Local Similarity 100.0%; Pred. No. 0.00e+00;	
	Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	1 MRLPKLTLFWLWLDLEFICTVLGAPDLGQRPQCTRPGLAKAEKAPPLARNVFRP	60
QY	1 MRLPKLTLFWLWLDLEFICTVLGAPDLGQRPQCTRPGLAKAEKAPPLARNVFRP	60
Db	61 GGHSGGGATNANAKGTTGOTGGLTOPKDEPKLPPRPGGPEKPGHPOTROTAR	120
QY	61 GGHSGGGATNANAKGTTGOTGGLTOPKDEPKLPPRPGGPEKPGHPOTROTAR	120
Db	121 TVTPKQLPGGKAPPKAGSVPSFLLLKAREPGPREPKPPPPITPHEYMLSLYRTL	180
QY	121 TVTPKQLPGGKAPPKAGSVPSFLLLKAREPGPREPKPPPPITPHEYMLSLYRTL	180
Db	181 SDADRKGSSVKLEAGLANTITSFIDKGDODRGPVVRKORYVFDISALEKGLLGAELR	240
QY	181 SDADRKGSSVKLEAGLANTITSFIDKGDODRGPVVRKORYVFDISALEKGLLGAELR	240





```
#journal      Development (1994) 120:209-218
#title        Bone morphogenetic proteins and a signalling pathway that
#             controls patterning in the developing chick limb.
#cross-references MUID:94163974
#accession    150608
##status      preliminary; translated from GB/EMBL/DBBJ
##molecule_type mRNA
##residues    1-405 ##label FRA
##cross-references EMBL:X75915; NID:g472929; PID:g472930
GENETICS
#gene         Bmp-4
CLASSIFICATION #superfamily inhibin
SUMMARY       #length 405 #molecular-weight 46057 #checksum 1371
Query Match   15.5%; Score 566; DB 2; Length 405;
Best Local Similarity 32.2%; Pred.No. 2.69e-80;
Matches 130; Conservative 89; Mismatches 152; Indels 33; Gaps 27;
D 23 HASLIPETGRKVAELQAGSGRRSAQSHLLRGFTTLLQMFGLRRRP-QPSKSA-VI 80
Q 110 HPQTRQATRTVP-KQLPGGRAPKAGSVPSFLKKAREPGPREPKEPFPPIIT 168
D 81 P-STYMLDYLRLQSGEERISLQSLQYSPERSARANTVRSFHHEHLESVPGPSEAPRI 139
Q 169 PHEYMLSLYRTL-S-DADKKGNSSVKL-E--AGLANITITSFDIKGQ-DD-RGPV-VRKQ 220
D 140 RFVNLSVDPNEVSSLEELRYREQVEEPSAAMERGFHRINIYEVKPLSERSQAITRL 199
Q 221 RYVFDISAL-EKDLGLGAEILRLKKPSDTAKPAAPGGGAAQLKLSGSGR-OPAS-L 277
D 200 LDTLRVH-HNVTRETVDVSPAVIRWTKDPNHLVTI-E---VTHLHQAQ-THUGKVR 253
Q 278 LDVRSVPLDGGSGWEVDFIWKLFNFNSAQICLELEAWERGRAVDLGLGFDRAARQVH 337
D 254 I-SRSLPGHGGDMAQL-RPLLVTFGHDGRG-HA-L-T-RRARSP--KHHGSR--KN-K 302
Q 338 EKALFLVFGRTKKDLFFNEIKARSGQDDKTVYEVLFESORRRRAPLATRQGRPSKNLK 397
D 303 KNCRRHALYVDFSDVGNWDIVAPPGYAFYCHGDCFPPLADHLNSTHAIIVQTLVNSVN 362
Q 398 ARCSRKALHVNFKDGMWDWIAPLEYEAFHCEGLCEFPPLSHLEPTNHAVIQTLMNSMD 457
D 363 S-STPKACCVPTELSALSMLYLDENEKVLKNYQDMVVEGCGCR 405
Q 458 PESPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501
#journal      Development (1994) 120:209-218
#title        Bone morphogenetic proteins and a signalling pathway that
#             controls patterning in the developing chick limb.
#cross-references MUID:94163974
#accession    150608
##status      preliminary; translated from GB/EMBL/DBBJ
##molecule_type mRNA
##residues    1-405 ##label FRA
##cross-references EMBL:X75915; NID:g472929; PID:g472930
GENETICS
#gene         Bmp-4
CLASSIFICATION #superfamily inhibin
SUMMARY       #length 405 #molecular-weight 46057 #checksum 1371
Query Match   14.9%; Score 544; DB 2; Length 393;
Best Local Similarity 32.7%; Pred.No. 4.23e-76;
Matches 112; Conservative 88; Mismatches 114; Indels 29; Gaps 26;
D 72 VVPP-YMLDLYRRHSGQGPALAPOHRLERASRANTVLSFHHEEIAEISELSMGKTSRRF 130
```

```
QY 167 ITPHEYMLSLYRTL-S-DADKKGNSSVKLEAGLANITITSFT-DKGQDDRGPPV-RK-QRY 222
DB 131 FPNLSSVPTDEFLTSABELOIFREOMQALGNSSFOHRINIYEIIKIPATASSKFPVTRLDD 190
QY 223 VFDISALEKDGGLL-GAELIRLKKPSDT-AKPAAPGGGAAQLKLSGSGRQAS-LDD 279
DB 191 TRLVTQ-NTSQWESFDVTPAVMRWTAOHTNHHGFVV-EVAHLEKPGVS-KRHVR-1-SR 245
QY 280 VRSVPLDGGSGWEVDFIWKLFNFNSAQICLELEAWERGRAVDLGLGFDRAARQVHEK 339
DB 246 SLHODEHSWSQVRPLL--V-T-FGHDGK-HP-L--HKREKR-Q-A-KH-KQR-KRLKS 291
QY 340 ALFL-VFGRTKKRDLEFNEIKARSGQDDKTVYEVLFESORRRRAPLATRQGRPSKNLKA 398
DB 292 SCKRHPLVDFSDVGNWDIVAPPGYAFYCHGDCFPPLADHLNSTHAIIVQTLVNSVNS 351
QY 399 RCSRKALHVNFKDGMWDWIAPLEYEAFHCEGLCEFPPLSHLEPTNHAVIQTLMNSMDP 458
DB 352 K-IPKACCVPTELSALSMLYLDENEKVLKNYQDMVVEGCGCR 393
QY 459 ESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501
RESULT      9
ENTRY       BMH02
TITLE       bone morphogenetic protein 2 precursor - human
ALTERNATE_NAMES
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change
05-Sep-1997
ACCESSIONS  B37278; PC2178
REFERENCE    A37278
#authors     Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mittleman, B.;
#journal     Science (1988) 242:1528-1534
#title       Novel regulators of bone formation: molecular clones and
            activities
#cross-references MUID:89072730
#accession   B37278
#molecule_type mRNA
#residues    1-396 ##label WO2
#cross-references GB:M22489; NID:g179501; PID:g179502
REFERENCE    PC2178
#authors     Ishida, N.; Tsujimoto, M.; Kanaya, T.; Shimamura, A.;
            M.; Nakanishi, T.; Kobayashi, J.; Nakazato, H.
#journal     J. Biochem. (1994) 115:279-285
#title       Expression and characterization of human bone morphogenetic
            protein-2 in silkworm larvae infected with recombinant
            Bombyx mori nuclear polyhedrosis virus.
#accession   PC2178
#molecule_type protein
#residues    290-295,'X',297-304 ##label ISH
#experimental_source cell line BOMo-15A1C
REFERENCE    A56729
#authors     Rathore, S.; Hammerstone, K.M.; Dansereau, S.; Porter, T.J.
#journal     Protein Sci. (1995) 4[Suppl.2]:443S
#title       N-terminal isoforms of recombinant human bone morphogenetic
            protein (rhBMP-2) are active in vitro and in vivo.
#contents    annotation
#note        determination of amino ends of mature forms; dimers with long
            form chains have reduced activity
COMMENT      This hormone is capable of inducing bone formation at ectopic
            morphological locations.
GENETICS
#gene        GDB:BMP2; BMP2A
#cross-references GDB:125204; OMIM:112261
#map_position 20p12-20p12
COMPLEX      homodimer, disulfide linked
CLASSIFICATION #superfamily inhibin
KEYWORDS     bone; dimer; glycoprotein; pyroglyutamic acid
FEATURE
```

```
1-23 #domain signal sequence #status predicted #label SIG\
24-265 #domain propeptide #status predicted #label PRO\
266-396 #product bone morphogenetic protein 2, long form #status
      predicted #label MATL\
283-396 #product bone morphogenetic protein 2 #status predicted
      #label MAT\
135,163,164,200 #binding_site carbohydrate (Asn) (covalent) #status
      predicted\
283 #modified_site pyrrolidone carboxylic acid (Gln) (in
      mature form) #status experimental\
338 #binding_site carbohydrate (Asn) (covalent) #status
      experimental
SUMMARY #length 396 #molecular-weight 44702 #checksum 9850
Query Match 14.9%; Score 546; DB 1; Length 396;
Best Local Similarity 31.1%; Pred. No. 1.76e-76;
Matches 119; Conservative 100; Mismatches 131; Indels 33; Gaps 29;
Db 37 SSGRPSQPSDEVLSFELRLLSMFLGKQRP-PSRDA-VVPP-YMLDLYRRHSQPGSP 93
Q 129 PGKAPPKAGS-VPSFLKKAREPGPPREPKEPPFPPTPHEYMLSLYRTLS-DADRK 186
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
Db 94 APDHLRAASRANTVRSFHHEESLEELPETSQKTRRRFFNLSISPTFEFITSAELOVF 153
Q 187 GGNSSVKLEAGLANTITSFI-DKGDD-RGPVVRK-QRYVFDISALEKDGLL-GAELRIL 242
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
Db 154 REQMDALGNSSPHHRIINIEIKPATANSKEPVTLLDTRLV-NQNASRWESFDVTPA 212
Q 243 RKPSDPAKPAAPGGGAA--OLKSLSCPSGROPAS-LLDVRSVPGDGGSGWEVFDIWLK 299
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
Db 213 VMRWTAQAHNGFV-EVAHLEKQGS-KRHYR-I-SRSLQDEHSWSQIRPLL--V 265
Q 300 FRNFKNSAQCLELEAWERGRAVDRLGLGFDRAARQVHEKALFL-VGRTKKRDLFFNEI 358
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
Db 266 -T-FGHDKG-HP-L--HKREKR-Q-A-KH-KQR-KRLKSSCRHPLVDFSDVGWMDWI 314
Q 359 KARSQDDKTVEYLFQSQRKRRAPLATROGKPSKRLKARCSKALHVNFKDMGWDWI 418
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
Db 315 VAPPGYHAFYCHGCPPLADHLNSTHAIQTLVNSVNSK-IPKACCVPTSELSAISM 373
Q 419 IAPLEYEAFHCEGLCEPLSHLEPTNHAIVQTLNLSMDPESTPTCCVPTRLSPISILF 478
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
Db 374 LDENEKVLKNYQDMVVEGCGCR 396
Q 479 IDSANNVYKQYEDMVVESCGR 501
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
```

```
RESULT 10 JH0687 #type complete
ENTRY bone morphogenetic protein 2I precursor - African clawed frog
TITLE #formal_name Xenopus laevis #common_name African clawed frog
ORGANISM 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
DATE 08-Sep-1997
ACCESSIONS JH0687 S16244
REFERENCE #authors Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
#journal Biochem. Biophys. Res. Commun. (1992) 186:1487-1495
#title Genes for bone morphogenetic proteins are differentially
      transcribed in early amphibian embryos.
#cross-references MUID:92378616
#accession JH0687
#molecule_type mRNA
#residues 1-398 #label NIS
#cross-references GB:X63424; NID:g64585; PID:g64586
#experimental_source oocyte
REFERENCE S16244
#authors Plessow, S.; Koester, M.; Knoechel, W.
#journal Biochim. Biophys. Acta (1991) 1089:280-282
#title cDNA sequence of Xenopus laevis bone morphogenetic protein 2
      (BMP-2).
#cross-references MUID:91274367
#accession S16244
#molecule_type mRNA
```

```
##residues 1-6,'S','8-15,'V','17-232,'N','234-398 #label PLE
##cross-references EMBL:X55031; NID:g64581; PID:g64582
CLASSIFICATION #superfamily inhibin
KEYWORDS dimer; glycoprotein
FEATURE
285-398 #product bone morphogenetic protein 2I #status predicted
      #label MAT\
137,202,340 #binding_site carbohydrate (Asn) (covalent) #status
      predicted
SUMMARY #length 398 #molecular-weight 45586 #checksum 9563
Query Match 14.9%; Score 544; DB 2; Length 398;
Best Local Similarity 32.7%; Pred. No. 4.23e-76;
Matches 126; Conservative 88; Mismatches 136; Indels 35; Gaps 28;
Db 36 SGRSSPQOSRVNLQFELRLLSMFLGKARRPT-PGKNVVIPP--YMLDLYHLHLAQLAADE 92
Q 130 GKGAPPKAG-SVPSFLLKKAREPGPPREPKEPPFPPTPHEYMLSLYRT-LSADARKG 187
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
Db 93 GTSAMDQMERAAASRANTVRSFHHEESMEETPESREKTIOEFFNLSISIPNEELVTSAE 152
Q 188 GNSV--KLE--AGLANTITSFI-DKGDD-RGPVVRK-QRYVFDISALEKDGLL-GAEL 239
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
Db 153 RIFREQQEPFESDKLHRIINIVKPAASARGPVVRLDTRLVH-HNESKWESFDV 211
Q 240 RILRKPSDTAKPAAPGGGAAQLKL--SSCPSGROPAS-SLDDVRSVPGDGGSGWEVFDI 296
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
Db 212 -TPAIA-RWIAH---K-QP-NHGFEVVEVTHLDNKNVKKHVR-ISRSLPTDKDNWFOIR 263
Q 297 WKLFNFKNSAQCLELEAWERGRAVDRLGLGFDRAARQVHEKALFLVFGRTKKRDLFFN 356
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
Db 264 PLLVTFSHDKG-HA-L--HKRQR-Q-A-RH-QQR-KRLKSSCRHPLVDFSDVGWMD 314
Q 357 EIKARSQDDKTVEYLFQSQRKRRAPLATROGKPSKRLKARCSKALHVNFKDMGWD 416
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
Db 315 WIVAPPYHAFYCHGCPPLADHLNSTHAIQTLVNSVNTN-IPKACCVPTSELSAISM 373
Q 417 WIAPLEYEAFHCEGLCEPLSHLEPTNHAIVQTLNLSMDPESTPTCCVPTRLSPISI 476
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
Db 374 LYDENKVLKNYQDMVVEGCGCR 398
Q 477 LFIDSANNVYKQYEDMVVESCGR 501
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
```

```
RESULT 11 I49542 #type complete
ENTRY bone morphogenetic protein 5 - mouse
TITLE #formal_name Mus musculus #common_name house mouse
ORGANISM 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
DATE 23-Feb-1997
ACCESSIONS I49542
REFERENCE I49542
#authors King, J.A.; Marker, P.C.; Seung, K.J.; Kingsley, D.M.
#journal Dev. Biol. (1994) 166:112-122
#title BMP5 and the molecular, skeletal, and soft-tissue alterations
      in short ear mice.
#cross-references MUID:95046894
#accession I49542
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-452 #label RES
#cross-references GB:L41145; NID:g755033; PID:g755034
GENETICS
#gene BMP5
CLASSIFICATION #superfamily inhibin
SUMMARY #length 452 #molecular-weight 51511 #checksum 1308
Query Match 14.9%; Score 546; DB 2; Length 452;
Best Local Similarity 28.8%; Pred. No. 1.76e-76;
Matches 107; Conservative 101; Mismatches 140; Indels 24; Gaps 23;
Db 94 PEEYLVR-VSLAGEAKETKGYASP-NGYAHRLHLPPRTPLTTQSPPLASLHDTNFD 151
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
      :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|::: :|:::
```

```

QY 141 PSSFLKKAREPGPPREPKEPPFPPTTIPHEYMSLY-RT-LS-DADRKGGNSVVKLEAG 197
Db 152 -ADMVMSFVNVLVERDKDFSHORRHYKEFRFDLTQIPHGEAVTAAEFRYKDKGNHRFENE 210
QY 198 LANTITSFIDKQDDRG-PVVRKQ-R-YVFDISALEK-DGLLGAELRLKPKSDTAKPA 253
Db 211 TIKIS-IYQI-IKEY-TNRDADLELDTTRKQALD-VGWLVFDTITVTSNHWVINPONNLG 266
QY 254 APGGRAAQLKSLSCPSGRQPA-SLLDVRSPVGLDGSWEVFDIWKLFNRF-KNS-AQLC 310
Db 267 LQCAETGDRGSRINVSAGLV-GRHGPQSQKPMW-AFFKASEVLLRSVRAAKRNQNR 324
QY 311 LEL-EAWERGRAVDLRLGDFDRAARQVHEKALEFLVGRTKKRDLEFNEIKARSGQDDKT 369
Db 325 NKS-SHQDPSRP-SA-GDYNTSEKQACKKHELYVSRDLGWQDWIITAPGYAAYC 380
QY 370 YEYLFQRRRRAPLATRQGRKPSKRLKARCSKALHVNFKDMGWDDWIIAPLEYEAFHC 429
Db 381 DGCSPFLNAHMNATHAIQVTLVHLMFDPKPCAPTCLNAISVLYFDDSSNWLK 440
QY 430 EGLCEFLRSHLEPETHAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQ 489
Db 441 YRNMVVRSCGCH 452
QY 490 YEDMVVESCGR 501

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ORGANISM #formal_name Homo sapiens #common_name man
DATE 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Sep-1998
ACCESSION A39263
REFERENCE Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.;
#authors Rosen, V.; Wang, E.A.; Wozney, J.M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:9843-9847
#title Identification of transforming growth factor beta family
members present in bone-inductive protein purified from
bovine bone.
#cross-references MIM:91088608
#accession A39263
#molecule_type mRNA
#residues 1-454 #label CEL
#cross-references GB:M60314; GB:N38693; NID:g339559; PID:g339560
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KEYWORDS bone; glycoprotein
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1-17
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317-454
#domain signal sequence #status predicted #label sig\
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#product bone morphogenetic protein 5 #status predicted
#label MAT\
211,327,345,395 #binding_site carbohydrate (Asn) (covalent) #status
predicted
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Best Local Similarity 30.8%; Pred.No. 6.56e-76;
Matches 96; Conservative 88; Mismatches 108; Indels 20; Gaps 18;

Db 154 ADMVMSFVNVLVERDKDFSHORRHYKEFRFDLTQIPHGEAVTAAEFRYKDRSNRNFENET 213
QY 199 ANTITFIDKQDDRG-PVVRKQ-R-YVFDISALEK-DGLLGAELRLKPKSDTAKPA 254
Db 214 IKIS-IYQI-IKEY-TNRDADLELDTTRKQALD-VGWLVFDTITVTSNHWVINPONNLG 269
QY 255 PGGGRAAQLKSLSCPSGRQPA-SLLDVRSPVGLDGSWEVFDIWKLFNRF-KNS-AQLCL 311

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Db 270 QLCAETGDRGSRINVSAGLV-VGRGPQSQKPMW-AFFKASEVLLRSVRAAKRNQNR 326
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Db 443 YRNMVVRSCGCH 454
QY 490 YEDMVVESCGR 501

RESULT 13
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TITLE bone morphogenetic protein-2 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 10-Dec-1994 #sequence_revision 17-Nov-1995 #text_change 03-May-1996
ACCESSION S45355
REFERENCE Mundy, G.R.; Harris, M.A.; Ghosh-Choudhury, N.; Feng, M.;
#authors Mundy, G.R.; Harris, S.E.
#journal Biochim. Biophys. Acta (1994) 1218:221-224
#title Structure and sequence of mouse bone morphogenetic protein-2
gene (BMP-2): comparison of the structures and promoter
regions of BMP-2 and BMP-4 genes.
#cross-references MIM:94289485
#accession S45355
#status preliminary
#molecule_type DNA
#residues 1-394 #label FEN
CLASSIFICATION #superfamily inhibin
SUMMARY #length 394 #molecular_weight 44509 #checksum 1098
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Best Local Similarity 55.2%; Pred.No. 5.24e-74;
Matches 64; Conservative 25; Mismatches 25; Indels 2; Gaps 2;

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QY 387 RQGR-RPSKRLKARCSKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEPPLRSHLEPTN 445
Db 340 HAIQVTLVNSVNSK-IPKACCVPTLSAISMVLYDENKVLKYNQDMVVGCGCR 394
QY 446 HAVIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501

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ENTRY JH0688 #type complete
TITLE bone morphogenetic protein 2II precursor - African clawed
frog
ORGANISM #formal_name Xenopus laevis #common_name African clawed frog
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Sep-1997
ACCESSION JH0688
REFERENCE Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
#authors Biochem. Biophys. Res. Commun. (1992) 186:1487-1495
#journal Genes for bone morphogenetic proteins are differentially
transcribed in early amphibian embryos.
#cross-references MIM:92378616
#accession JH0688
#molecule_type mRNA
#residues 1-398 #label NIS
#cross-references GB:X63425; NID:g64583; PID:g64584
#experimental_source oocyte
CLASSIFICATION #superfamily inhibin
KEYWORDS glycoprotein

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WORLD (TM)

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Release 3.1A John F. Collins, Biocomputing Research Unit.  
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Distribution rights by Oxford Molecular Ltd

MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Apr 19 19:52:19 2000; MasPar time 10.53 Seconds  
Far output not generated. 632.638 Million cell updates/sec

Title: >US-09-297-092-1  
Description: (1-501) from US09297092.pep  
Perfect Score: 3662  
Sequence: 1 MRLPKLLTFLMVLAWLDE.....ANNVYKQYEDMWVESCGR 501

Scoring table: PAM 150  
Gap 11

Searched: 134018 seqs, 13297625 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-issued  
1:5A\_COMB 2:5B\_COMB 3:6\_COMB 4: PCT9\_COMB 5:backfiles1

Statistics: Mean 34.368; Variance 167.251; scale 0.205

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description	Pred. No.
1	3662	100.0	501	2	US-08-288-	Sequence 2, Applicatio	0.00e+00
2	3332	91.0	495	1	US-08-455-	Sequence 10, Applicati	1.15e-278
3	3332	91.0	495	4	PCT-US94-0	Sequence 10, Applicati	1.15e-278
4	904	24.7	120	1	US-08-362-	Sequence 4, Applicatio	2.05e-65
5	904	24.7	120	4	PCT-US94-1	Sequence 4, Applicatio	2.05e-65
6	903	24.7	321	4	PCT-US94-1	Sequence 26, Applicati	2.50e-65
7	903	24.7	321	1	US-08-362-	Sequence 26, Applicati	2.50e-65
8	895	24.4	119	1	US-08-455-	Sequence 13, Applicati	1.23e-64
9	895	24.4	119	4	PCT-US94-0	Sequence 13, Applicati	1.23e-64
10	849	23.2	263	1	US-08-362-	Sequence 32, Applicati	1.14e-60
11	849	23.2	263	4	PCT-US94-1	Sequence 32, Applicati	1.14e-60
12	832	22.7	134	4	PCT-US94-0	Sequence 6, Applicatio	3.32e-59
13	832	22.7	134	1	US-08-581-	Sequence 6, Applicatio	3.32e-59
14	815	22.3	388	4	PCT-US94-1	Sequence 34, Applicati	9.63e-58
15	815	22.3	388	1	US-08-362-	Sequence 34, Applicati	9.63e-58
16	795	21.7	411	1	US-08-362-	Sequence 28, Applicati	5.05e-56
17	795	21.7	411	4	PCT-US94-1	Sequence 28, Applicati	5.05e-56
18	790	21.6	119	1	US-08-581-	Sequence 7, Applicatio	1.36e-55
19	790	21.6	119	4	PCT-US94-0	Sequence 7, Applicatio	1.36e-55
20	784	21.4	102	2	US-08-288-	Sequence 13, Applicati	4.45e-55
21	784	21.4	102	1	US-08-335-	Sequence 51, Applicati	4.45e-55
22	741	20.2	129	1	US-08-360-	Sequence 15, Applicati	2.18e-51
23	741	20.2	129	1	US-08-741-	Sequence-13, Applicati	2.18e-51

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CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (202)638-5000
CC TELEFAX: (202)638-4810
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 501 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 501 AA; 55410 MW; 1235559 CN;

Query Match      100.0%; Score 3662; DB 2; Length 501;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GGHYGGGATNANARAGGTGGLTQPKKDEPKKLPDRPGGPKPGHPQTRQATAR 120
121 TVTPKGLPGGKAPPKAGSVPSFLKKAREPPPPREPFRPPPTPHEYMLSLYRTL 180
QY 121 TVTPKGLPGGKAPPKAGSVPSFLKKAREPPPPREPFRPPPTPHEYMLSLYRTL 180
181 SDARKKGNSSVKLEAGLANITITFDKGQDDRGPAVRKQRYVFDISALEKDGLLGAE 240
QY 181 SDARKKGNSSVKLEAGLANITITFDKGQDDRGPAVRKQRYVFDISALEKDGLLGAE 240
241 ILRKPPSDTAKPAAPGGGAAQLSSCPGROPAASLLDVRSPGLDGSWEVFDINKLF 300
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QY 301 RNFKNQAQLCLEAWERGRAVDLRLGLGFDRAARQVHEKALFLVFGRTKKRDLEFFNEIKA 360
361 RSGQDDKTVEYLFSSQRRKRAPLATRQGRPSKNLARC SRKALHVNFKDMGDDWIIA 420
QY 361 RSGQDDKTVEYLFSSQRRKRAPLATRQGRPSKNLARC SRKALHVNFKDMGDDWIIA 420
421 PLEYEAFHCEGLCEFFPLRSHLEPTNHAVIOTLMNSMDPESTPTCCVTRLSILFID 480
QY 421 PLEYEAFHCEGLCEFFPLRSHLEPTNHAVIOTLMNSMDPESTPTCCVTRLSILFID 480
481 SANNVYKQYEDMVVESGCR 501
QY 481 SANNVYKQYEDMVVESGCR 501

RESULT 2
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AC xxxxxx
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DT
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Sequence 10, Application US/08455559
CC Patent No. 5801014
CC GENERAL INFORMATION:
CC APPLICANT: LEE, SE-JIN
CC APPLICANT: HUYNH, THANH
CC TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
CC NUMBER OF SEQUENCES: 27
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
CC STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CC CITY: LOS ANGELES
CC STATE: CALIFORNIA
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CC COUNTRY: US
CC ZIP: 90067
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/455,559
CC FILING DATE: 31-MAY-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/003,144
CC FILING DATE: 12-JAN-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: WETHERELL, JR. PH.D., JOHN R.
CC REGISTRATION NUMBER: 31,678
CC REFERENCE/DOCKET NUMBER: PD2280
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619/455-5100
CC TELEFAX: 619-455-5110
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 495 amino acids
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Matches 457; Conservative 23; Mismatches 15; Indels 6; Gaps 2;

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355 RSGQDDKTVEYLFSSQRRKRAPLATRQGRPSKNLARC SRKALHVNFKDMGDDWIIA 414
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415 PLEYEAFHCEGLCEFFPLRSHLEPTNHAVIOTLMNSMDPESTPTCCVTRLSILFID 474
QY 421 PLEYEAFHCEGLCEFFPLRSHLEPTNHAVIOTLMNSMDPESTPTCCVTRLSILFID 480
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$\ddot{O}$

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CC  
GENERAL INFORMATION:  
CC  
APPLICANT: SE-JIN LEE  
CC  
APPLICANT: HUYNH, THANH  
CC  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5  
CC  
NUMBER OF SEQUENCES: 27  
CC  
CORRESPONDENCE ADDRESS:  
CC  
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ  
CC  
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR  
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CITY: LOS ANGELES  
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STATE: CALIFORNIA  
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COUNTRY: US  
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ZIP: 90067  
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COMPUTER READABLE FORM:  
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COMPUTER: IBM PC compatible  
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OPERATING SYSTEM: PC-DOS/MS-DOS  
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SOFTWARE: PatentIn Release #1.0, Version #1.25  
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CURRENT APPLICATION DATA:  
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APPLICATION NUMBER: PCT/US94/00657  
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FILING DATE: 1/12/94  
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CLASSIFICATION:  
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ATTORNEY/AGENT INFORMATION:  
CC  
NAME: WETHERELL, JR. PH.D., JOHN R.  
CC  
REGISTRATION NUMBER: 31,678  
CC  
REFERENCE/DOCKET NUMBER: FD3256 CIP OF PD2280  
CC  
TELEPHONE: 619/455-5100  
CC  
TELEFAX: 619/455-5110  
CC  
INFORMATION FOR SEQ ID NO: 13:  
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SEQUENCE CHARACTERISTICS:  
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LENGTH: 119 amino acids  
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TYPE: amino acid  
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STRANDEDNESS: single  
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Matches 118; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
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QY 443 PTNHAVIOTLMSNDPSTPTCCVPTRLSPISILFIDSANNVYKQYEDMVVESCGR 501  
  
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Sequence 32, Application US/08362670B  
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Sequence 32, Application US/08362670B  
CC  
Patent No. 5658882  
CC  
GENERAL INFORMATION:  
CC  
APPLICANT: Celeste, Anthony J.  
CC  
APPLICANT: Wozney, John  
CC  
APPLICANT: Rosen, Vicki A.  
CC  
APPLICANT: Wolfman, Neil  
CC  
APPLICANT: Thomsen, Gerald H.  
CC  
APPLICANT: Melton, Douglas A.  
CC  
TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS  
CC  
NUMBER OF SEQUENCES: 37  
CC  
CORRESPONDENCE ADDRESS:  
CC  
ADDRESSEE: GENETICS INSTITUTE, INC.  
CC  
STREET: 87 Cambridgepark Drive  
CC  
CITY: Cambridge  
CC  
STATE: Massachusetts  
CC  
COUNTRY: USA  
CC  
ZIP: 02140  
CC  
COMPUTER READABLE FORM:  
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MEDIUM TYPE: Floppy disk  
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COMPUTER: IBM PC compatible  
CC  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CC  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC  
CURRENT APPLICATION DATA:  
CC  
APPLICATION NUMBER: US/08/362,670B  
CC  
FILING DATE: December 22, 1994  
CC  
CLASSIFICATION: 514  
CC  
ATTORNEY/AGENT INFORMATION:  
CC  
NAME: Lazar, Steven R.  
CC  
REGISTRATION NUMBER: 32,618  
CC  
REFERENCE/DOCKET NUMBER: 5202-D  
CC  
TELEPHONE: 617 498-8260  
CC  
TELEFAX: 617 876-5851  
CC  
INFORMATION FOR SEQ ID NO: 32:  
CC  
SEQUENCE CHARACTERISTICS:  
CC  
LENGTH: 263 amino acids  
CC  
TYPE: amino acid  
CC  
TOPOLOGY: linear  
CC  
MOLECULE TYPE: protein  
CC  
SQ SEQUENCE 263 AA; 29183 MW; 354042 CN;  
  
Query Match 23.2%; Score 849; DB 1; Length 263;  
Best Local Similarity 59.8%; Pred. No. 1.14e-60;  
Matches 119; Conservative 41; Mismatches 25; Indels 14; Gaps 10;  
  
Db 65 QQPPDLRLSIFGGRVRRPQERALLVVFTRSORKNLFTMHHEOLGSAAGAAGSCGPAP 124  
QY 317 ERGRAVDLRLGDFDRAARQVHERKALFLVFGTRKRDLF--FNE-I-KARS-GQDDK--T- 368  
Db 125 SGSPDGTGSLPSPGRRRRRTAFASRHGKRGKSRKRLHVNFKELGWDWIITAPL 184  
QY 369 V-Y-E--YLFQ-RRRRAPLATROGKRPSSKLNKARCSRKALHVNFKMDGWDWIITAPL 422  
Db 185 EYEAHYCEGVCDPLRSHLEPTNHAIITQTLMSNDPSTPTCCVPTRLSPISILYDAG 244  
QY 423 EYEAHFCEGLCEFPRLRSHLEPTNHAVIOTLMSNDPSTPTCCVPTRLSPISILFIDS 482  
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QY 483 NNXYKQYEDMVVESCGR 501  
  
RESULT 11  
ID PCT-US94-14030A-32 STANDARD; PRT; 263 AA.

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AC  
XX  
DT  
XX  
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xxxxxx

Sequence 32, Application PC/TUS9414030A

Sequence 32, Application PC/TUS9414030A

GENERAL INFORMATION:

APPLICANT: GENETICS INSTITUTE, INC.

APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE

TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENETICS INSTITUTE, INC.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/14030A

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/164,103

FILING DATE: 07-DEC-1993

APPLICATION NUMBER: US 08/217,780

FILING DATE: 25-MAR-1994

APPLICATION NUMBER: US 08/333,576

FILING DATE: 02-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Lazar, Steven R.

REGISTRATION NUMBER: 32,618

REFERENCE/DOCKET NUMBER: 5202D-PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617 498-8260

TELEFAX: 617 876-5851

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 263 AA; 29183 MW; 354042 CN;

Query Match

Best Local Similarity 23.2%; Score 849; DB 4; Length 263;

Matches 119; Conservative 41; Mismatches 25; Indels 14; Gaps 10;

Db 65 QPPPLDLRLSLGFGRRVPPQBRALLVVFTRSORKNLFEMHEQLGSAEAGSCGAP 124

QY 317 ENGRAVDLGLGFDRAAQVHEKALFVGRYKKDLP--FNE-I-KARS-QQDK--T- 368

Db 125 SGSPDTGWLPSGRRRRRTAFASRGHGRKSRKPLHVNFKELGWDWIIAPL 184

QY 369 V-Y-E--YLFQ--RRKRAPLATRGKRPKNLARCSTRKALHVNFKDGMGWDWIIAPL 422

Db 185 EYEATHCEGVCDFPLRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPTISILYIDAG 244

QY 423 EYEAFCGCLCEFPRLRSHLEPTNHAIQTLMNSMDPESTPTCCVPTRLSPISILFIDSA 482

Db 245 NNXYVYQYEDMVEGCGR 263

QY 483 NNXYVYQYEDMVEGCGR 501

RESULT 12

ID  
XX  
AC  
XX  
DT  
XX  
XX

PCT-US94-07762-6

STANDARD;

PRT; 134 AA.

xxxxxx

Sequence 6, Application PC/TUS9407762

Sequence 6, Application PC/TUS9407762

GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Spensley Horn Jubas & Lubitz

STREET: 1880 Century Park East, Suite 500

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/07762

FILING DATE: 08-JUL-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: TUMARKIN, LISA A., PH.D.

REGISTRATION NUMBER: P-38,347

REFERENCE/DOCKET NUMBER: ED2349

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 455-5100

TELEFAX: (619) 455-5110

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 134 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 134 AA; 15226 MW; 97138 CN;

Query Match

Best Local Similarity 22.7%; Score 832; DB 4; Length 134;

Matches 99; Conservative 22; Mismatches 4; Indels 0; Gaps 0;

Db 10 RRRRTAFASRGHGRKSRKPLHVNFKELGWDWIIAPLEYAYHCEGVCDFF 69

QY 377 RRKRAPLATRGKRPKNLARCSTRKALHVNFKDGMGWDWIIAPLEYAFHCEGLCEFP 436

Db 70 LRSHLEPTNHAIQTLMNSMDPGSTPPSCCVPTKLTPTISILYIDAGNNVYVYQYEDMVE 129

QY 437 LRSHLEPTNHAIQTLMNSMDPESTPTCCVPTRLSPISILFIDSANNVYVYQYEDMVE 496

Db 130 SCGR 134

QY 497 SCGR 501

RESULT 13

ID US-08-581-529B-6

STANDARD;

PRT; 134 AA.

xxxxxx

Sequence 6, Application US/08581529B

Sequence 6, Application US/08581529B

Patent No. 577044

GENERAL INFORMATION:





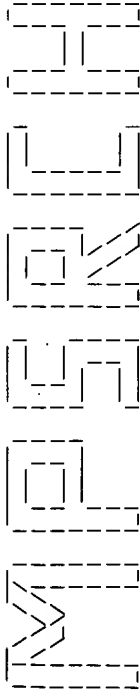
CC APPLICANT: Celeste, Anthony J.  
CC APPLICANT: Wozney, John  
CC APPLICANT: Rosen, Vicki A.  
CC APPLICANT: Wolfman, Neil  
CC APPLICANT: Thomsen, Gerald H.  
CC APPLICANT: Melton, Douglas A.  
CC TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS  
CC NUMBER OF SEQUENCES: 37  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: GENETICS INSTITUTE, INC.  
CC STREET: 87 Cambridgepark Drive  
CC CITY: Cambridge  
CC STATE: Massachusetts  
CC COUNTRY: USA  
CC ZIP: 02140  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/362,670B  
CC FILING DATE: December 22, 1994  
CC CLASSIFICATION: 514  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Lazar, Steven R.  
CC REGISTRATION NUMBER: 32,618  
CC REFERENCE/DOCKET NUMBER: 5202-D  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 617 498-8260  
CC TELEFAX: 617 876-5851  
CC INFORMATION FOR SEQ ID NO: 34:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 388 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 388 AA; 42118 MW; 683274 CN;

Query Match 22.3%; Score 815; DB 1; Length 388;  
Best Local Similarity 45.0%; Pred. No. 9.63e-58;  
Matches 147; Conservative 84; Mismatches 60; Indels 36; Gaps 20;  
Db 65 RSPADESAETGSGFLFDVSSLNDADVVGAELVLRGSGPESG-PGSWTS--PPLLLLS 121  
QY 208 KGODRGVVRKQRYVFDISAL-EKDLGLGAELRLDKKPSDTAKPAAPGGRAAQLKUS 266  
Db 122 TCGAARAPRLLYSRAAEPLVGQRWEAFDVADAMRRHRREPRPPRAFCLLLRAVAGVPS 181  
QY 267 SCPSGRQPASLLDVRSPGLDGSWEVFDIWK-LFRNFKN--AQ-LCLELEA-WERGRA 321  
Db 182 PLALRLGFGWPGGSGSAEERAVLVVSSRTORKESLFRFIRAQARALGAALASEPLDPP 241  
QY 322 -VDRLGLGFDRAA---RQVHEKALFLVFGRTKKRLDFNEIKA--RS-GQ----D---D- 366  
Db 242 GTGTASPRAVIGRRRRRTALACTRTAOGSGGACGCHGRGRSRSRKLPHVDFKELGW 301  
QY 367 -K-TYTE-YLFSORRRRAPLA-TR--QOK-----R-PSKNLKARCSRKALHVNFKDMGW 414  
Db 302 DDMITAPLEYAYHCGIGCDFPLRSHLEPTNHAITQTLNLSMAPDAAPASCVCVPARLSPI 361  
QY 415 DDMITAPLEYAYHCGIGCDFPLRSHLEPTNHAITQTLNLSMAPDAAPASCVCVPARLSPI 474  
Db 362 SILYIDAANNVYKQYEDMVVEACGCR 388  
QY 475 SILFIDSANNVYKQYEDMVVEACGCR 501

Search completed: Wed Apr 19 19:52:44 2000  
Job time : 25 secs.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Wed Apr 19 19:50:05 2000; MasPar time 35.99 Seconds  
329.759 Million cell updates/sec  
Your output not generated.

Title: >US-09-297-092-1  
Description: (1-501) from US09297092.pep  
Perfect Score: 3662  
Sequence: 1 MRLPKLLTFLWYLAWLDE.....ANNVYKQYEDMVVESCGR 501

Scoring table: PAM 150  
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq36  
1:geneseqp

Statistics: Mean 36.609; Variance 166.724; scale 0.220

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Description	ID	Length	Pred. No.
1	3662	100.0	TGF-beta superfamily s	W44868	501	0.00e+00
2	3662	100.0	Human MP52 protein.	W01799	501	0.00e+00
3	3662	100.0	Human high mol. wt. pr	W11900	501	0.00e+00
4	3662	100.0	Human bone morphogenetic	W12770	501	0.00e+00
5	3662	100.0	New TGF-beta family me	R69600	501	0.00e+00
6	3662	100.0	Human MP52.	W36100	501	0.00e+00
7	3662	100.0	Human MP52.	W33008	501	0.00e+00
8	3662	100.0	Human TGF-beta protein	W19210	501	0.00e+00
9	3608	98.5	Cartilage-derived morp	R95635	501	0.00e+00
10	3332	91.0	Growth differentiation	R60022	495	9.21e-297
11	2925	79.9	TGF-beta-like clone MP	R40800	401	2.39e-258
12	939	25.6	Cartilage-derived morp	R95636	436	2.00e-72
13	904	24.7	Human MP52 protein.	W26590	420	3.33e-69
14	904	24.7	Murine protein MP52.	R78731	120	3.33e-69
15	903	24.7	Human bone morphogenet	W26591	321	4.12e-69
16	903	24.7	Human mature VL-1 (BMP	R78730	321	4.12e-69
17	900	24.6	Human MP52 growth fact	W06920	119	7.77e-69
18	900	24.6	Human bone inducing fa	W19846	119	7.77e-69
19	856	23.4	Murine mv2 protein.	R78739	263	8.59e-65
20	856	23.4	Murine BMP-13 homologo	W26595	263	8.59e-65
21	832	22.7	GDF-6.	R66867	134	1.37e-62
22	815	22.3	Human bone morphogenet	R78734	388	4.95e-61
23	815	22.3	Human bone morphogenet	W26592	388	4.95e-61

ALIGNMENTS

RESULT 1

ID W44868 standard; protein; 501 AA.

AC W44868;

DT 24-SEP-1998 (first entry)

DE TGF-beta superfamily subunit.

KW TGF-beta; calcium phosphate matrix; bioactive implant; parodontosis;

KW bone replacement; cartilage; bone; fracture.

OS Synthetic.

PN DE19647853-A1.

PD 20-MAY-1998.

PF 19-NOV-1996; 047853.

PR 19-NOV-1996; DE-047853.

PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.

PA GMBH BIOMATERIALS & MEDICAL.

PI Heide H, Pabst J, Paulista M, Pohl J;

DR WPI; 98-287890/26.

PT Bioactive implant material for bone replacement - comprising

PT osteogenic calcium phosphate matrix coated with protein

PS Claim 3; Page 8-10; 12pp; German.

CC The TGF-beta superfamily subunit can be used together with a calcium

CC phosphate matrix to produce a bioactive implant material for bone

CC replacement. The implant has cartilage and/or bone-forming activity and

CC can be used for local treatment of cartilage and/or bone diseases or

CC damage caused by trauma, surgery, degeneration or overloading. The

CC implant can also be used for the treatment of bone defects, e.g.

CC parodontosis or fractures and in cosmetic and plastic surgery for fixing

CC mobile bones.

SQ Sequence 501 AA;

Query Match 100.0%; Score 3662; DB 1; Length 501;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MRLPKLLTFLWYLAWLDEFTCTVLGAPDLGQRPGTGLAKAKAKPRPLARNVFRP 60

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Db 61 GGHSYGGATNANARAKGTGTGGLTOPKDEPKKLPKPPGPGPKPGHPQTRQATAR 120

QY 61 GGHSYGGATNANARAKGTGTGGLTOPKDEPKKLPKPPGPGPKPGHPQTRQATAR 120

Db 121 TVTPKGQLPGGKAPKAGSVSPSSFLKKAREPGPPREPKEPPRPPIPTPHEYMLSLYRTL 180

QY 121 TVTPKGQLPGGKAPKAGSVSPSSFLKKAREPGPPREPKEPPRPPIPTPHEYMLSLYRTL 180

Db 181 SDADRKGNSSVKLEAGLANTITSFDKQDDRGPPVRKQRYVFDISALEKGLLGAELR 240

QY 181 SDADKGGNSSVKLEAGLANITITSFDKQDDRGVVRKQRYVFDISALEKDGGLGAEIR 240  
 DB 241 ILRKKPSDTAKPAAPGGGAAQLKSSCPGROPASLLDVRSPGLDGSWEVFDIWKLF 300  
 QY 241 ILRKKPSDTAKPAAPGGGAAQLKSSCPGROPASLLDVRSPGLDGSWEVFDIWKLF 300  
 DB 301 RNFNSAQLCLELEAWERGRAVDLRLGLGFDRAARQVHEKALFLVFGRTKKRDLEFNEIKA 360  
 QY 301 RNFNSAQLCLELEAWERGRAVDLRLGLGFDRAARQVHEKALFLVFGRTKKRDLEFNEIKA 360  
 DB 361 RSGODDKTVVYELFSQRRKRRAPIATROGKRPSKNLARCASKALHVNFKDMGDDWIIA 420  
 QY 361 RSGODDKTVVYELFSQRRKRRAPIATROGKRPSKNLARCASKALHVNFKDMGDDWIIA 420  
 DB 421 PLEYEAHFCEGLCEFFPLRSHLEPTNHAVIOTLMNSMDPESTPPTCCVPTRLSPISILFID 480  
 QY 421 PLEYEAHFCEGLCEFFPLRSHLEPTNHAVIOTLMNSMDPESTPPTCCVPTRLSPISILFID 480  
 DB 481 SANNVYKQYEDMVVESCGR 501  
 QY 481 SANNVYKQYEDMVVESCGR 501

RESULT 2  
 ID W01799 standard; Protein; 501 AA.  
 AC W01799;  
 DT 15-OCT-1997 (first entry)  
 DE Human MP52 protein.  
 KW Human; MP52; transforming growth factor; TGF; beta; medicament;  
 KW treatment; prevention; nervous system; disease; neuropathology;  
 KW ageing.  
 OS Homo sapiens.  
 PN DE19525416-AL.  
 PD 16-JAN-1997.  
 PF 12-JUL-1995; DE-025416.  
 PR 12-JUL-1995; DE-025416.  
 PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.  
 PI Bechtold R, Hoetten G, Paulista M, Pohl J, Unsicker K;  
 DR WPI; 97-078343/08.  
 JR N-PSDB; T59405.  
 PT Medicaments contg. protein MP52 - useful for treating neurological disorders  
 PS Claim 2: Pages 12-14; 21pp; German.  
 CC The present sequence is the human MP52 protein, which is described in WO 9316099 and 9504819 as a member of the human transforming growth factor beta superfamily. Active MP52 can be used in a medicament to treat and prevent nervous system diseases, and/or to treat neuropathological conditions caused by nervous system ageing.  
 CC system ageing.  
 SQ Sequence 501 AA;

Query Match 100.0%; Score 3662; DB 1; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 MRLPKLLTFLWYLAWLDELICIVLGPDLGQRPQGTGRLGAKAEKERPLARNVFRP 60  
 QY 1 MRLPKLLTFLWYLAWLDELICIVLGPDLGQRPQGTGRLGAKAEKERPLARNVFRP 60  
 DB 61 GHSYGGGATNANARAKGTTGOTGLTOPKKDEPKLPPRPGGPEPKHPPTQATAR 120  
 QY 61 GHSYGGGATNANARAKGTTGOTGLTOPKKDEPKLPPRPGGPEPKHPPTQATAR 120  
 DB 121 TVTPKGQLPGKAPPKAGSVPSFLLKKAREPPPPREPKEPPPTIPHEYMLSLYRTL 180  
 QY 121 TVTPKGQLPGKAPPKAGSVPSFLLKKAREPPPPREPKEPPPTIPHEYMLSLYRTL 180  
 DB 181 SDADKGGNSSVKLEAGLANITITSFDKQDDRGVVRKQRYVFDISALEKDGGLGAEIR 240  
 QY 181 SDADKGGNSSVKLEAGLANITITSFDKQDDRGVVRKQRYVFDISALEKDGGLGAEIR 240  
 DB 241 ILRKKPSDTAKPAAPGGGAAQLKSSCPGROPASLLDVRSPGLDGSWEVFDIWKLF 300

QY 241 ILRKKPSDTAKPAAPGGGAAQLKSSCPGROPASLLDVRSPGLDGSWEVFDIWKLF 300  
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 QY 301 RNFNSAQLCLELEAWERGRAVDLRLGLGFDRAARQVHEKALFLVFGRTKKRDLEFNEIKA 360  
 DB 361 RSGODDKTVVYELFSQRRKRRAPIATROGKRPSKNLARCASKALHVNFKDMGDDWIIA 420  
 QY 361 RSGODDKTVVYELFSQRRKRRAPIATROGKRPSKNLARCASKALHVNFKDMGDDWIIA 420  
 DB 421 PLEYEAHFCEGLCEFFPLRSHLEPTNHAVIOTLMNSMDPESTPPTCCVPTRLSPISILFID 480  
 QY 421 PLEYEAHFCEGLCEFFPLRSHLEPTNHAVIOTLMNSMDPESTPPTCCVPTRLSPISILFID 480  
 DB 481 SANNVYKQYEDMVVESCGR 501  
 QY 481 SANNVYKQYEDMVVESCGR 501

RESULT 3  
 ID W11900 standard; Protein; 501 AA.  
 AC W11900;  
 DT 28-OCT-1997 (first entry)  
 DE Human high mol. wt. protein MP52, a growth/differentiation factor.  
 KW Growth factor; differentiation; bone induction; osteoporosis; teeth;  
 KW tooth; dental; joint tissue; cartilage; mucous membrane; skin; nails;  
 KW wound healing; regeneration; skeletal disorder; fracture; dimer.  
 OS Homo sapiens.  
 PN W09704095-AL.  
 PD 06-FEB-1997.  
 PF 24-JUL-1996; J02065.  
 PR 24-JUL-1995; JP-218022.  
 PA (FARH) HOECHST JAPAN LTD.  
 PI Fujino Y, Kawai S, Kimura M, Matsumoto T, Takahashi M;  
 DR WPI; 97-132636/12.  
 JR N-PSDB; T61412.  
 PT High molecular weight human MP52 growth or differentiation factor - promotes bone induction; is useful for treatment and prevention of bone disease  
 PS Claim 1; Page 12-16; 25pp; Japanese.  
 CC W11900 is a high mol. wt. form of a human growth/differentiation factor MP52. MP52 promotes bone induction and is useful for plastic reconstructive surgery, cosmetic facial treatment, bone transplantation and tooth implantation. It is also useful for the treatment and prevention of disorders of bone formation, bone, cartilage, joint tissue, skin, mucous membranes, nails or teeth; for wound treatment and tissue regeneration; and for the treatment of skeletal disorders and fractures.  
 CC regeneration; and for the treatment of skeletal disorders and fractures.  
 SQ Sequence 501 AA;

Query Match 100.0%; Score 3662; DB 1; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 DB 61 GHSYGGGATNANARAKGTTGOTGLTOPKKDEPKLPPRPGGPEPKHPPTQATAR 120  
 QY 61 GHSYGGGATNANARAKGTTGOTGLTOPKKDEPKLPPRPGGPEPKHPPTQATAR 120  
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 QY 121 TVTPKGQLPGKAPPKAGSVPSFLLKKAREPPPPREPKEPPPTIPHEYMLSLYRTL 180  
 DB 181 SDADKGGNSSVKLEAGLANITITSFDKQDDRGVVRKQRYVFDISALEKDGGLGAEIR 240  
 QY 181 SDADKGGNSSVKLEAGLANITITSFDKQDDRGVVRKQRYVFDISALEKDGGLGAEIR 240  
 DB 241 ILRKKPSDTAKPAAPGGGAAQLKSSCPGROPASLLDVRSPGLDGSWEVFDIWKLF 300



Best Local Similarity 100.0%; Score 3662; DB 1; Length 501;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 1 MRLPKLLTFLWYLAWLDEFICTVLGAPDLGQRPQGTREGLAKAEAKERPPLARNVFRP 60

Db 61 GHSYGGGATNANARAKGTTGQGLTQPKKDEPKLPPRPGGPEPKPGHPPTQQTAR 120  
 QY 61 GHSYGGGATNANARAKGTTGQGLTQPKKDEPKLPPRPGGPEPKPGHPPTQQTAR 120

Db 121 TVTPKGOLPGKAPPKAGSVPSFLLKKAREPGPPREPKEPFRPPPTTPHEYMLSLYRTL 180  
 QY 121 TVTPKGOLPGKAPPKAGSVPSFLLKKAREPGPPREPKEPFRPPPTTPHEYMLSLYRTL 180

Db 181 SDADKGGNSVLEAGLANTITSFIDKGQDDRGPPVVRKQRYVFDISALEKDGLLGAELR 240  
 QY 181 SDADKGGNSVLEAGLANTITSFIDKGQDDRGPPVVRKQRYVFDISALEKDGLLGAELR 240

Db 241 ILRKKPSDTAKPAAPGGGAAQLKSSCPGROPASLLDVSVPGLDGSWEVFDIWKLF 300  
 QY 241 ILRKKPSDTAKPAAPGGGAAQLKSSCPGROPASLLDVSVPGLDGSWEVFDIWKLF 300

Db 301 RNFKNQAQLCLELEAWERGRAVDLRLGLGFDRAAQVHEKALFLVFGRTKKRDLFFNEIKA 360  
 QY 301 RNFKNQAQLCLELEAWERGRAVDLRLGLGFDRAAQVHEKALFLVFGRTKKRDLFFNEIKA 360

Db 361 RSGQDDKTVYEIFSQRKRRAPLAPLQGRKPSKNLKAHVNFKDMGDDWIIA 420  
 QY 361 RSGQDDKTVYEIFSQRKRRAPLAPLQGRKPSKNLKAHVNFKDMGDDWIIA 420

Db 421 PLEYAFHCEGLCEFFLRSHLEPTNHAVIOTLMSMDPESTPTCCVPTRLSPISILFID 480  
 QY 421 PLEYAFHCEGLCEFFLRSHLEPTNHAVIOTLMSMDPESTPTCCVPTRLSPISILFID 480

Db 481 SANNVYKQYEDMVVESCGR 501  
 QY 481 SANNVYKQYEDMVVESCGR 501

RESULT 6  
 ID W36100 standard; Protein; 501 AA.  
 AC W36100;  
 DT 08-MAY-1998 (first entry)  
 DE Human MP52.  
 KW Bone morphogenetic protein; BMP; processing enzyme; MP52;  
 KW BMP-2; BMP-4; BMP-6; BMP-7; bone formation; bone regeneration.  
 OS Homo sapiens.  
 PN WO9741250-A1.  
 PD 06-NOV-1997.  
 PF 28-APR-1997; J01474.  
 PR 30-APR-1996; JP-130618.  
 PA (FARH ) HOECHST YAKUHIN KOGYO KK.  
 PA (FARH ) HOECHST PHARM & CHEM KK.  
 PI Kimura M, Makishima F, Takahashi M;  
 DR WPI: 97-549748/50.  
 DR N-PSDB; T98191.  
 PT Production of mature bone morphogenetic protein - by treatment of  
 PT precursor protein with a processing enzyme such as furin either  
 PT directly or by expressing them both in the same host  
 PS Example 1; Pages 21-25; 34pp; Japanese.  
 CC The present sequence is MP52, which is a bone morphogenetic  
 CC protein (BMP).  
 CC Mature BMP can be produced by directly adding a BMP processing  
 CC enzyme to a solution containing BMP precursor protein, or by  
 CC transforming an animal cell with expression vectors containing DNA  
 CC encoding the enzyme and precursor protein, culturing the  
 CC transformant and isolating the mature BMP from the culture. The  
 CC method can be used to produce MP52, BMP-2, BMP-4, BMP-6 and BMP-7,  
 CC which can be used to treat bone formation or regeneration  
 CC abnormalities.  
 SQ Sequence 501 AA;

Query Match 100.0%; Score 3662; DB 1; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MRLPKLLTFLWYLAWLDEFICTVLGAPDLGQRPQGTREGLAKAEAKERPPLARNVFRP 60  
 QY 1 MRLPKLLTFLWYLAWLDEFICTVLGAPDLGQRPQGTREGLAKAEAKERPPLARNVFRP 60

Db 61 GHSYGGGATNANARAKGTTGQGLTQPKKDEPKLPPRPGGPEPKPGHPPTQQTAR 120  
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Db 121 TVTPKGOLPGKAPPKAGSVPSFLLKKAREPGPPREPKEPFRPPPTTPHEYMLSLYRTL 180  
 QY 121 TVTPKGOLPGKAPPKAGSVPSFLLKKAREPGPPREPKEPFRPPPTTPHEYMLSLYRTL 180

Db 181 SDADKGGNSVLEAGLANTITSFIDKGQDDRGPPVVRKQRYVFDISALEKDGLLGAELR 240  
 QY 181 SDADKGGNSVLEAGLANTITSFIDKGQDDRGPPVVRKQRYVFDISALEKDGLLGAELR 240

Db 241 ILRKKPSDTAKPAAPGGGAAQLKSSCPGROPASLLDVSVPGLDGSWEVFDIWKLF 300  
 QY 241 ILRKKPSDTAKPAAPGGGAAQLKSSCPGROPASLLDVSVPGLDGSWEVFDIWKLF 300

Db 301 RNFKNQAQLCLELEAWERGRAVDLRLGLGFDRAAQVHEKALFLVFGRTKKRDLFFNEIKA 360  
 QY 301 RNFKNQAQLCLELEAWERGRAVDLRLGLGFDRAAQVHEKALFLVFGRTKKRDLFFNEIKA 360

Db 361 RSGQDDKTVYEIFSQRKRRAPLAPLQGRKPSKNLKAHVNFKDMGDDWIIA 420  
 QY 361 RSGQDDKTVYEIFSQRKRRAPLAPLQGRKPSKNLKAHVNFKDMGDDWIIA 420

Db 421 PLEYAFHCEGLCEFFLRSHLEPTNHAVIOTLMSMDPESTPTCCVPTRLSPISILFID 480  
 QY 421 PLEYAFHCEGLCEFFLRSHLEPTNHAVIOTLMSMDPESTPTCCVPTRLSPISILFID 480

Db 481 SANNVYKQYEDMVVESCGR 501  
 QY 481 SANNVYKQYEDMVVESCGR 501

RESULT 7  
 ID W33008 standard; Protein; 501 AA.  
 AC W33008;  
 DT 22-MAY-1998 (first entry)  
 DE Human MP52.  
 KW Human MP52; mouse monoclonal antibody; MAB; purification;  
 KW assayng.  
 OS Homo sapiens.  
 FH Key  
 FT Peptide 1..27 Location/Qualifiers  
 FT /label= sig\_peptide  
 FT 28..501  
 FT /label= mat\_peptide  
 PN WO9743408-A1.  
 PD 20-NOV-1997.  
 PF 13-MAY-1997; J01603.  
 PR 07-MAY-1997; JP-131631.  
 PR 13-MAY-1996; JP-141137.  
 PA (FARH ) HOECHST PHARM & CHEM KK.  
 PI Jitsukawa T, Kitagawa H, Nakagawa H, Yanagisawa S;  
 DR WPI: 98-008877/01.  
 DR N-PSDB; T88340.  
 PT Mouse anti-human MP52 monoclonal antibody - recognises the dimeric  
 PT form of MP52 but not the monomer, and does not cross-react with  
 PT TGF-beta or BMP-2  
 PS Disclosure; Pages 31-35; 46pp; Japanese.  
 CC The present sequence, human MP52, was used in the  
 CC preparation of a novel mouse monoclonal antibody (MAB), which  
 CC recognises dimeric but not monomeric human MP52. The MAB has a  
 CC heavy chain of subclass gamma, and does not cross-react with  
 CC TGF-beta or BMP-2. The MAB may be used to purify and assay human  
 CC MP52, especially recombinant MP52.